

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 7, 2005, 11:40:59 ; Search time 64.8455 Seconds  
(without alignments)  
1864.305 Million cell updates/sec

Title: US-10-726-721A-9

Perfect score: 1715

Sequence: 1 RGDVDDAGDCSGARYNDWSD.....VKVGKEMAKLAEHMFPKSQE 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1713	99.9	337	4	AAG67776	Aag67776 Amino aci
2	1708	99.6	342	4	AAB27240	Aab27240 Human EXM
3	1708	99.6	342	7	ADJ69028	Adj69028 Human hea
4	1708	99.6	379	4	AAU12279	Aau12279 Human PRO
5	1708	99.6	379	4	AAB68359	Aab68359 Amino aci
6	1708	99.6	379	4	AAM40083	Aam40083 Human pol
7	1708	99.6	379	6	ABO17723	Abo17723 Novel hum
8	1708	99.6	379	6	ABU80977	Abu80977 Human PRO
9	1708	99.6	379	6	ABU66677	Abu66677 Human PRO

10	1708	99.6	379	6	ABU59758	Abu59758 Novel sec
11	1708	99.6	379	6	ABO24948	Abo24948 Human sec
12	1708	99.6	379	6	ABU66953	Abu66953 Human sec
13	1708	99.6	379	6	ADA45735	Ada45735 Novel hum
14	1708	99.6	379	6	ADA76166	Ada76166 Human PRO
15	1708	99.6	379	6	ADA18816	Ada18816 Human PRO
16	1708	99.6	379	6	ADA61439	Ada61439 Homo sapi
17	1708	99.6	379	6	ADB19224	Adb19224 Novel hum
18	1708	99.6	379	6	ADB27765	Adb27765 Human PRO
19	1708	99.6	379	6	ADA86244	Ada86244 Novel hum
20	1708	99.6	379	6	ADB15808	Adb15808 Human PRO
21	1708	99.6	379	6	ADA47594	Ada47594 Human PRO
22	1708	99.6	379	6	ADA67389	Ada67389 Human PRO
23	1708	99.6	379	6	ADB30396	Adb30396 Human PRO
24	1708	99.6	379	6	ADA85692	Ada85692 Novel hum
25	1708	99.6	379	6	ADA96904	Ada96904 Human PRO
26	1708	99.6	379	6	ADA79208	Ada79208 Human PRO
27	1708	99.6	379	6	ADA87347	Ada87347 Novel hum
28	1708	99.6	379	6	ADB16549	Adb16549 Human PRO
29	1708	99.6	379	6	ADA91641	Ada91641 Novel hum
30	1708	99.6	379	6	ADB14704	Adb14704 Human PRO
31	1708	99.6	379	6	ADB18665	Adb18665 Novel hum
32	1708	99.6	379	6	ADA93880	Ada93880 Human PRO
33	1708	99.6	379	6	ADB19776	Adb19776 Novel hum
34	1708	99.6	379	6	ADB13088	Adb13088 Human PRO
35	1708	99.6	379	6	ABO43256	Abo43256 Novel hum
36	1708	99.6	379	6	ADA74342	Ada74342 Human PRO
37	1708	99.6	379	6	ADB24575	Adb24575 Human PRO
38	1708	99.6	379	6	ADA82099	Ada82099 Human PRO
39	1708	99.6	379	6	ADA75062	Ada75062 Human PRO
40	1708	99.6	379	6	ADA85140	Ada85140 Novel hum
41	1708	99.6	379	6	ADA84588	Ada84588 Novel hum
42	1708	99.6	379	6	ADB29844	Adb29844 Human PRO
43	1708	99.6	379	6	ADA80372	Ada80372 Human PRO
44	1708	99.6	379	6	ADA75614	Ada75614 Human PRO
45	1708	99.6	379	6	ADA46839	Ada46839 Human PRO

#### ALIGNMENTS

#### RESULT 1

AAG67776

ID AAG67776 standard; protein; 337 AA.

XX

AC AAG67776;

XX

DT 10-DEC-2001 (first entry)

XX

DE Amino acid sequence of a human FE65 binding PTB1 domain protein.

XX

KW Human; phosphotyrosine binding domain 1; PTB1 domain; FE65; beta-amyloid; Alzheimer's disease; FEBP1; FE65 binding PTB1 domain protein; hnRNPL; neurodegenerative disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers  
FT Misc-difference 305  
FT /note= "unspecified residue encoded by GNT"  
XX  
PN WO200159104-A1.  
XX  
PD 16-AUG-2001.  
XX  
PF 07-FEB-2001; 2001WO-FR000361.  
XX  
PR 10-FEB-2000; 2000FR-00001628.  
PR 18-APR-2000; 2000US-0198500P.  
XX  
PA (AVET ) AVENTIS PHARMA SA.  
XX  
PI Maury I, Mercken L, Fournier A;  
XX  
DR WPI; 2001-589717/66.  
DR N-PSDB; AAH78615.  
XX  
PT Compound capable of modulating interaction between the PTB1 domain of  
PT FE65 protein and hnRNPL and/or FEBP1 protein, useful to treat  
PT neurological disorders including Alzheimer's disease.  
XX  
PS Claim 9; Page 42-43; 5lpp; French.  
XX  
CC The present sequence represents a human FEBP1 (FE65 binding PTB1 domain  
CC protein). The protein is a partner of the human FE65 protein. FE65 is  
CC implicated in the production of beta-amyloid. Partners of the FE65  
CC protein thus represent novel targets for the treatment of Alzheimer's  
CC disease. Such partners include FEBP1 and hnRNPL (undefined). Compounds  
CC which are capable of at least partially modulating interactions between  
CC hnRNPL and/or FEBP1 proteins or their homologues and the phosphotyrosine  
CC binding domain 1 (PTB1) domain of FE65 are used to treat  
CC neurodegenerative diseases. In particular, they are used for treating  
CC Alzheimer's disease  
XX  
SQ Sequence 337 AA;

Query Match 99.9%; Score 1713; DB 4; Length 337;  
Best Local Similarity 100.0%; Pred. No. 2.2e-162;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRAR 60  
| |||||||  
Db 1 RGDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRAR 60

Qy 61 RAVQKRASPNSDDTVLSPQELQKVLCLEMSEKPYILEAALIALGNNAAYAFNRDIIRDL 120  
| |||||||  
Db 61 RAVQKRASPNSDDTVLSPQELQKVLCLEMSEKPYILEAALIALGNNAAYAFNRDIIRDL 120

Qy 121 GGLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQL 180  
| |||||||  
Db 121 GGLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQL 180

Qy 181 AGLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLNLAEVPAMTRELLR 240  
| |||||||

Db 181 AGLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLNLAENPAMTRELLR 240  
Qy 241 AQVSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQV 300  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 241 AQVSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQV 300  
Qy 301 CADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 301 CADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337

RESULT 2

AAB27240

ID AAB27240 standard; protein; 342 AA.

XX

AC AAB27240;

XX

DT 27-MAR-2001 (first entry)

XX

DE Human EXMAD-18 SEQ ID NO: 18.

XX

KW Extracellular matrix and adhesion-associated protein; EXMAD; cancer;  
KW inflammation; reproductive disorder; cardiovascular disorder;  
KW immune disorder; musculoskeletal disorder; developmental disorder;  
KW gastrointestinal disorder; cell proliferation disorder.

XX

OS Homo sapiens.

XX

PN WO200068380-A2.

XX

PD 16-NOV-2000.

XX

PF 10-MAY-2000; 2000WO-US012811.

XX

PR 11-MAY-1999; 99US-0133643P.

PR 23-AUG-1999; 99US-0150409P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Bandman O, Hillman JL, Tang YT, Lal P, Yue H, Baughn MR, Lu DAM;  
PI Azimzai Y;

XX

DR WPI; 2001-007395/01.

DR N-PSDB; AAC66907.

XX

PT Isolated polynucleotide encoding extracellular matrix or adhesion-  
PT associated protein (EXMAD) useful for diagnosing, treating, or preventing  
PT disorders associated with expression of EXMAD such as proliferative,  
PT immune and genetic disorders.

XX

PS Claim 1; Page 105-106; 129pp; English.

XX

CC The present invention provides the protein and coding sequences for 25  
CC novel extracellular matrix and adhesion-associated proteins (EXMADs).  
CC These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-5, EXMAD-  
CC 6, EXMAD-7, EXMAD-8, EXMAD-9, EXMAD-10, EXMAD-11, EXMAD-12, EXMAD-13,  
CC EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-18, EXMAD-19, EXMAD-20,

CC EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24 and EXMAD-25. They are useful in  
CC the prevention and treatment of cancers, cell proliferation,  
CC cardiovascular, reproductive, immune, musculoskeletal, developmental and  
CC gastrointestinal disorders and inflammation

XX

SQ Sequence 342 AA;

Query Match 99.6%; Score 1708; DB 4; Length 342;  
Best Local Similarity 99.7%; Pred. No. 7.2e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
Db 7 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 66

Qy 62 AVQKRASPNSDDTVLSPQELQVKLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 67 AVQKRASPNSDDTVLSPQELQVKLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 126

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
Db 127 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 186

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
Db 187 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA 246

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
Db 247 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 306

Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
Db 307 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 342

RESULT 3

ADJ69028

ID ADJ69028 standard; protein; 342 AA.

XX

AC ADJ69028;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human heat mitochondrial protein as a therapeutic target SeqID834.

XX

KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytostatic.

XX

OS Homo sapiens.

XX

PN WO2003087768-A2.

XX  
PD 23-OCT-2003.  
XX  
PF 04-APR-2003; 2003WO-US010870.  
XX  
PR 12-APR-2002; 2002US-0372843P.  
PR 17-JUN-2002; 2002US-0389987P.  
PR 20-SEP-2002; 2002US-0412418P.  
XX  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX  
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
XX  
DR WPI; 2003-845369/78.  
XX  
PT Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX  
PS Claim 1; SEQ ID NO 834; 180pp; English.  
XX  
CC This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nootropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytostatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX  
SQ Sequence 342 AA;

Query Match 99.6%; Score 1708; DB 7; Length 342;  
Best Local Similarity 99.7%; Pred. No. 7.2e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 61  
Db 7 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 66

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 67 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 126

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 181  
Db 127 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 186

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLNLAEVPAMTRELLRA 241  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 187 GLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLNLAEVPAMTRELLRA 246

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 247 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 306

Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
||| ||| ||| ||| ||| ||| ||| |||  
Db 307 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 342

RESULT 4

AAU12279

ID AAU12279 standard; protein; 379 AA.

XX

AC AAU12279;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human PRO6007 polypeptide sequence.

XX

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
KW A-peptide; factor VIIA; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200140466-A2.

XX

PD 07-JUN-2001.

XX

PF 01-DEC-2000; 2000WO-US032678.

XX

PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 09-DEC-1999; 99US-0170262P.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.

PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2001-408281/43.

DR N-PSDB; AAS21351.

XX

PT Isolated , secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
PT breast, prostate, cervical.

XX

PS Claim 12; Fig 216; 813pp; English.

XX

CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO  
CC polypeptides. The PRO polypeptides are useful to detect other PRO  
CC polypeptides, to link bioactive molecules to cells expressing PRO  
CC polypeptides, to modulate biological activities of cells expressing PRO  
CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample. Some  
CC of the 275 sequences are also useful to stimulate the release of tumour  
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
CC differentiation of chondrocytes, the proliferation or gene expression in  
CC pericyte cells, the release of proteoglycans from cartilage, the  
CC proliferation of inner ear utricular supporting cells or of T-  
CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
CC involved in binding interactions. The polynucleotides encoding PRO  
CC polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy

XX

SQ Sequence 379 AA;

Query Match 99.6%; Score 1708; DB 4; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 283

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 301  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 343

Qy 302 ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 337  
Db 344 ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 379

RESULT 5

AAB68359

ID AAB68359 standard; protein; 379 AA.

XX

AC AAB68359;

XX

DT 09-JUL-2001 (first entry)

XX

DE Amino acid sequence of a human IkappaB kinase binding protein Y2H35.

XX

KW IkappaB kinase binding protein; IKK binding protein; Y2H35; inflammation;  
KW apoptosis; inflammatory mediator.

XX

OS Homo sapiens.

XX

PN US6214582-B1.

XX

PD 10-APR-2001.

XX

PF 16-NOV-1998; 98US-00193266.

XX

PR 16-NOV-1998; 98US-00193266.

XX

PA (UYNY ) UNIV NEW YORK STATE RES FOUND.

XX

PI Marcu KB;

XX  
DR WPI; 2001-315460/33.  
DR N-PSDB; AAF85219, AAF85220.  
XX  
PT Novel isolated nucleic acid molecule encoding isolated IkB kinase binding  
PT protein designated Y2H35, useful as probes and primers in molecular  
PT biology and biotechnology.  
XX  
PS Disclosure; Col 11-14; 10pp; English.  
XX  
CC The present sequence represents a human IkappaB kinase (IKK) binding  
CC protein, designated Y2H35. Fragments of Y2H35 polynucleotide are useful  
CC as probes and primers in molecular biology and biotechnology. The Y2H35  
CC protein is useful for elucidating and controlling pathways leading to  
CC inflammation and apoptosis, for detecting IKK complexes and modulating  
CC IKK activity in cells undergoing signalling by inflammatory mediator such  
CC as tumour necrosis factor alpha (TNFalpha) and interleukin-1 (IL-1), and  
CC for identifying therapeutically active agents that modulate the binding  
CC or interaction of Y2H35 and either IKKalpha or IKKbeta  
XX  
SQ Sequence 379 AA;

Query Match 99.6%; Score 1708; DB 4; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQVLCIVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 104 AVQKRASPNSDDTVLSPQELQVLCIVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 283

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKEEENEPTQNQFGEGLFFLKEFQVC 301  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKEEENEPTQNQFGEGLFFLKEFQVC 343

Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
Db 344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

RESULT 6  
AAM40083  
ID AAM40083 standard; protein; 379 AA.  
XX  
AC AAM40083;  
XX

DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 3228.  
XX  
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US034263.  
XX  
PR 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
DR WPI; 2001-442253/47.  
DR N-PSDB; AAI59239.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 5; SEQ ID NO 3228; 10078pp; English.  
XX  
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form

CC part of the printed specification

XX

SQ Sequence 379 AA;

Query Match 99.6%; Score 1708; DB 4; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 181  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 283

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343

Qy 302 ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 337  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 344 ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 379

RESULT 7

ABO17723

ID ABO17723 standard; protein; 379 AA.

XX

AC ABO17723;

XX

DT 26-AUG-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO6007.

XX

KW Human; secreted and transmembrane protein; PRO; antiinflammatory;  
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;  
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;  
KW TNF-alpha release; cell proliferation; cell differentiation;  
KW gene expression modulator; proteoglycan release; cytokine release;  
KW tumour; inflammatory disease; organ failure; atherosclerosis;  
KW cardiac injury; infertility; birth defect; premature aging; AIDS;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;  
KW bioreactor; tissue typing.

XX

OS Homo sapiens.

XX

PN US2003032156-A1.

XX  
PD 13-FEB-2003.  
XX  
PF 06-MAY-2002; 2002US-00140474.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.

PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2003-341980/32.

DR N-PSDB; ACD23960.

XX

PT New secreted and transmembrane PRO nucleic acids, for treating  
PT inflammation, organ failure, atherosclerosis, cardiac injury,  
PT infertility, birth defects, premature aging, axquired immunodeficiency  
PT syndrome (AIDS), or cancer.

xx

PS Claim 12; Fig 216; 660pp; English.

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The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a PRO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate the uptake of glucose or free fatty acid by cells, stimulate or inhibit the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The nucleic acid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide

xx

SO Sequence 379 AA;

```

Query Match          99.6%; Score 1708; DB 6; Length 379;
Best Local Similarity 99.7%; Pred. No. 8.3e-162;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

    2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 61
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
    44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 103
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
    62 AVQKRASPNSDDTVLSPQELOKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
    104 AVQKRASPNSDDTVLSPQELOKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163
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    122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 181
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | |
    164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 223
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | |
    182 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNLAENPAMTRELLRA 241
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | |
    224 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNLAENPAMTRELLRA 283
       ||||||| | | | | | | | | | | | | | | | | | | | | | | |
    242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 301
       ||||||| | | | | | | | | | | | | | | | | | | | | | | |
    284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 343
       ||||||| | | | | | | | | | | | | | | | | | | | | |
    302 ADKXLGIESHHDFLVKVKGKFMKAHLAEMFPKSQE 337

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Db

344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

RESULT 8

ABU80977

ID ABU80977 standard; protein; 379 AA.

XX

AC ABU80977;

XX

DT 23-JUN-2003 (first entry)

XX

DE Human PRO polypeptide #108.

XX

KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;  
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;  
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;  
KW hearing loss; coagulation disorder; stroke; heart attack; cardiant;  
KW antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;  
KW antirheumatic; auditory; cerebroprotective; angiogenic.

XX

OS Homo sapiens.

XX

PN US2003004311-A1.

XX

PD 02-JAN-2003.

XX

PF 19-DEC-2001; 2001US-00028072.

XX

PR 18-JUN-1997; 97US-0049911P.  
PR 26-AUG-1997; 97US-0056974P.  
PR 17-SEP-1997; 97US-0059113P.  
PR 17-SEP-1997; 97US-0059115P.  
PR 17-SEP-1997; 97US-0059117P.  
PR 17-SEP-1997; 97US-0059122P.  
PR 17-SEP-1997; 97US-0059184P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 19-SEP-1997; 97US-0059352P.  
PR 19-SEP-1997; 97US-0059588P.  
PR 24-SEP-1997; 97US-0059836P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 17-OCT-1997; 97US-0062285P.  
PR 17-OCT-1997; 97US-0062287P.  
PR 17-OCT-1997; 97US-0063755P.  
PR 24-OCT-1997; 97US-0062814P.  
PR 24-OCT-1997; 97US-0062816P.  
PR 24-OCT-1997; 97US-0063045P.  
PR 24-OCT-1997; 97US-0063082P.  
PR 24-OCT-1997; 97US-0063127P.  
PR 27-OCT-1997; 97US-0063327P.  
PR 27-OCT-1997; 97US-0063329P.  
PR 28-OCT-1997; 97US-0063550P.  
PR 28-OCT-1997; 97US-0063561P.  
PR 29-OCT-1997; 97US-0063704P.  
PR 29-OCT-1997; 97US-0063733P.  
PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.  
PR 03-NOV-1997; 97US-0064248P.  
PR 07-NOV-1997; 97US-0064809P.  
PR 12-NOV-1997; 97US-0065186P.  
PR 17-NOV-1997; 97US-0065846P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 24-NOV-1997; 97US-0066453P.  
PR 24-NOV-1997; 97US-0066511P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 11-DEC-1997; 97US-0069212P.  
PR 11-DEC-1997; 97US-0069278P.  
PR 11-DEC-1997; 97US-0069334P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 23-JAN-1998; 98US-0072320P.  
PR 04-FEB-1998; 98US-0073612P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2003-352836/33.

DR N-PSDB; ACA67101.

XX

PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid  
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or  
PT heart attack.

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PS Claim 12; Fig 216; 643pp; English.

XX

CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides and polynucleotides are useful for preparing a medicament  
CC useful in the treatment of diabetes, bone and/or cartilage disorders  
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,  
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders  
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic  
CC assays for PRO, by detecting its expression in specific cells, tissues or  
CC serum, and for affinity purification of PRO from recombinant cell culture  
CC or natural sources. ABU80870-ABU81144 represent the human PRO  
CC polypeptides of the invention. Note: The sequence data for this patent  
CC was obtained in electronic format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipsDIDEntry.html

XX

SQ Sequence 379 AA;

Query Match 99.6%; Score 1708; DB 6; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61

Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163  
  
Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223  
  
Qy 182 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 283  
  
Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343  
  
Qy 302 ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 337  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 344 ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 379

RESULT 9

ABU66677

ID ABU66677 standard; protein; 379 AA.

XX

AC ABU66677;

XX

DT 23-MAY-2003 (first entry)

XX

DE Human PRO polypeptide #108.

XX

KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.

XX

OS Homo sapiens.

XX

PN US2003036180-A1.

XX

PD 20-FEB-2003.

XX

PF 09-MAY-2002; 2002US-00143114.

XX

PR 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019094.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022991.

PR 29-OCT-1998; 98WO-US022992.

PR 20-NOV-1998; 98WO-US024855.

PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2003-332040/31.

DR N-PSDB; ACA03710.

XX

PT New secreted and transmembrane PRO nucleic acids, useful for gene  
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue  
PT typing, and in chromosome identification.

XX

PS Claim 12; Fig 216; 660pp; English.

XX

CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for identifying  
CC agonists or antagonists. The PRO polypeptides are useful for  
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from  
CC human blood, for stimulating the proliferation or differentiation of  
CC chondrocytes, and detecting the presence of tumours. The polynucleotide  
CC sequences encoding PRO polypeptides are useful as hybridisation probes,  
CC in chromosome and gene mapping, in the generation of antisense RNA and  
CC DNA, in the preparation of PRO polypeptides, for generating transgenic

CC animals or knockout animals, for the genetic analysis of individuals with  
CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the  
CC human PRO polypeptides of the invention. Note: The sequence data for this  
CC patent was obtained in electronic format directly from the USPTO web site  
CC at seqdata.uspto.gov/psipsDIDEntry.html

XX

SQ Sequence 379 AA;

Query Match 99.6%; Score 1708; DB 6; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	2	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	61
Db	44	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR	103
Qy	62	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
Db	104	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
Qy	122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	181
Db	164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	223
Qy	182	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA	241
Db	224	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA	283
Qy	242	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKEEENEPTQNQFGEGLFFFKEFQVC	301
Db	284	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKEEENEPTQNQFGEGLFFFKEFQVC	343
Qy	302	ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE	337
Db	344	ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE	379

RESULT 10

ABU59758

ID ABU59758 standard; protein; 379 AA.

XX

AC ABU59758;

XX

DT 13-MAY-2003 (first entry)

XX

DE Novel secreted and transmembrane protein PRO6007.

XX

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosum; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.

XX  
OS Homo sapiens.  
XX  
PN US2003017563-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 07-MAY-2002; 2002US-00140808.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX  
DR WPI; 2003-148238/14.  
DR N-PSDB; ABX89248.  
XX  
PT Two hundred and seventy five nucleic acids encoding PRO polypeptides,  
PT useful for treating pericyte-associated tumors, diabetes and various bone  
PT and/or cartilage disorders, e.g. arthritis.  
XX  
PS Claim 12; Fig 216; 659pp; English.  
XX  
CC The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpetiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and are  
CC thus useful for treating sports injuries, and arthritis. This is the  
CC amino acid sequence of a novel human PRO protein  
XX  
SQ Sequence 379 AA;

Query Match 99.6%; Score 1708; DB 6; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103  
  
Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163  
  
Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 181  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
| |||||||  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 283  
  
Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
| |||||||  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343  
  
Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
| |||  
Db 344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

RESULT 11

ABO24948

ID ABO24948 standard; protein; 379 AA.

XX

AC ABO24948;

XX

DT 05-SEP-2003 (first entry)

XX

DE Human secreted/transmembrane protein (PRO) #108.

XX

KW Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;  
KW gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;  
KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;  
KW PBMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;  
KW chondrocyte cell proliferation; chondrocyte cell differentiation;  
KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;  
KW endothelial cell; A-peptide; factor VIIA.

XX

OS Homo sapiens.

XX

PN US2003036179-A1.

XX

PD 20-FEB-2003.

XX

PF 10-MAY-2002; 2002US-00142431.

XX

PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2003-466355/44.

DR N-PSDB; ACD41902.

XX

PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or  
PT PRO4978, useful in molecular biology, chromosome and gene mapping, in  
PT generating antisense RNA and DNA, and in gene therapy.

XX

PS Claim 12; Fig 216; 659pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising at least 80%  
CC sequence identity to a PRO (secreted and transmembrane protein) cDNA  
CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its  
CC extracellular domain (with or without its associated signal peptide),  
CC which comprises any of the 275 120-850 residue amino acid sequences,  
CC given in the specification; (b) comprising any of the 275 300-3500  
CC nucleotide sequences, given in the specification; or (c) comprising the  
CC full-length coding sequence of the nucleotide sequences given in the  
CC specification, or of the DNA deposited under any of the American Type  
CC Culture Collection (ATCC) Accession Numbers listed in the specification.  
CC Also included are a vector comprising the novel nucleic acid, a host cell  
CC comprising the vector, producing a PRO polypeptide, the isolated PRO  
CC polypeptides detailed above, a chimaeric molecule comprising the PRO  
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO  
CC antibody, detecting a PRO polypeptide in a sample suspected of containing  
CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a

CC PRO polypeptide, modulating at least one biological activity of a cell  
CC expressing a PRO polypeptide, stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, (or proteoglycans from  
CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),  
CC modulating the uptake of glucose or FFA by skeletal muscle cells or  
CC adipocyte cells, stimulating the proliferation or differentiation of  
CC chondrocyte cells (or proliferation of or gene expression in pericyte  
CC cells), stimulating the proliferation of inner ear utricular supporting  
CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the  
CC binding of A-peptide to factor VIIA, or differentiation of adipocyte  
CC cells, detecting the presence of a tumour in a mammal and an  
CC oligonucleotide probe derived from any of the nucleotide sequences given  
CC in the specification. The polynucleotide is useful in molecular biology,  
CC including uses as hybridisation probes, in chromosome and gene mapping,  
CC in generating antisense RNA and DNA, and in gene therapy. The  
CC polynucleotide may also be used in preparing PRO polypeptides by  
CC recombinant techniques, and in generating either transgenic animals or  
CC knock-out animals which, in turn, are useful in the development and  
CC screening of therapeutically useful reagents. The PRO polypeptide or the  
CC antibody is used in preparing a medicament for treating a condition  
CC responsive to the polypeptide or antibody, such as tumours, and in  
CC various diagnostic assays. The present sequence represents a PRO  
CC polypeptide

xx

SO Sequence 379 AA:

Query Match 99.6%; Score 1708; DB 6; Length 379;  
 Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
 Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	61
44	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	103
62	AVQKRASPNSDDTVLSPQELQKVLCLEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
104	AVQKRASPNSDDTVLSPQELQKVLCLEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	181
164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	223
182	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLNLAEQPAMTRELLRA	241
224	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLNLAEQPAMTRELLRA	283
242	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	301
284	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	343
302	ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE	337
344	ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSOE	379

RESULT 12  
ABU66953

ID ABU66953 standard; protein; 379 AA.  
XX  
AC ABU66953;  
XX  
DT 27-MAY-2003 (first entry)  
XX  
DE Human secreted/transmembrane, PRO, protein SEQ ID 216.  
XX  
KW Human; secreted protein; transmembrane protein; PRO;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defects; premature aging; AIDS; biosensor;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW bioreactor; tumour.  
XX  
OS Homo sapiens.  
XX  
PN US2003032155-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 03-MAY-2002; 2002US-00137865.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.

PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

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PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2003-331925/31.

DR N-PSDB; ACA04131.

XX

PT New secreted and transmembrane nucleic acids and polypeptides, designated  
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,  
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or  
PT cancer.

XX

PS Claim 12; Fig 216; 659pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising, or which is  
CC at least 80% identical to, or the full-length coding sequence of, any of  
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
CC (one of 275 secreted or transmembrane proteins). The nucleic acid further  
CC comprises the full-length coding sequence of the DNA deposited under  
CC American Type Culture Collection (ATCC) accession number in a list given  
CC in the specification. Also included are vectors and host cells for  
CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO  
CC extracellular domains and mature sequences, methods of detecting PRO  
CC proteins, methods for stimulating the release of TNF-alpha (tumour  
CC necrosis factor alpha) from human blood, (and the proliferation of  
CC differentiation of chondrocyte cells, the proliferation of, or gene  
CC expression in pericyte cells, the release or proteoglycans from  
CC cartilage, proliferation of inner ear utricular supporting cells, the  
CC proliferation of T-lymphocyte cells, the release of a cytokine from  
CC peripheral blood mononuclear cells (PBMC), or the proliferation of  
CC endothelial cells), a method for modulating the uptake of glucose or free  
CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the  
CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte  
CC cells, a method for detecting the presence of a tumour in a mammal and an  
CC oligonucleotide probe derived from any of the nucleotide sequences cited  
CC above. The nucleic acids and polypeptides are useful for treating  
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,  
CC infertility, birth defects, premature aging, AIDS (acquired  
CC immunodeficiency syndrome), cancer, or diabetic complications. The  
CC nucleic acids are useful as hybridisation probes, in chromosome and gene  
CC mapping, and in generating antisense RNA or DNA. The polypeptides are  
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both  
CC are useful in tissue typing. The present sequence represents a PRO  
CC protein of the invention

XX

SQ Sequence 379 AA;

Query Match 99.6%; Score 1708; DB 6; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	2	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR	61
Db	44	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR	103
Qy	62	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
Db	104	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
Qy	122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	181
Db	164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	223
Qy	182	GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrellra	241
Db	224	GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrellra	283
Qy	242	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	301
Db	284	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	343
Qy	302	ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE	337
Db	344	ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE	379

RESULT 13

ADA45735

ID ADA45735 standard; protein; 379 AA.

XX

AC ADA45735;

XX

DT 20-NOV-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO6007.

XX

KW Human; secreted and transmembrane protein; PRO;  
KW Tumour necrosis factor alpha release; TNF-alpha release;  
KW glucose uptake modulator; FFA uptake modulator;  
KW cell proliferation stimulator; cell differentiation stimulator;  
KW cell differentiation inhibitor; cytokine release stimulator; tumour;  
KW lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;  
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;  
KW gene therapy; chromosome identification; chromosome marker.

XX

OS Homo sapiens.

XX

PN US2003022328-A1.

XX

PD 30-JAN-2003.

XX

PF 16-APR-2002; 2002US-00123904.

XX

PR 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2003-584997/55.

DR N-PSDB; ADA45734.

XX

PT Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers.

XX

PS Claim 12; Fig 216; 659pp; English.

XX

CC The invention describes 305 nucleic acids encoding PRO (secreted and  
CC transmembrane) polypeptides (I). (I) is useful for stimulating the  
CC release of TNF-alpha from human blood, for modulating the uptake of  
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for  
CC stimulating the proliferation or differentiation of chondrocyte cells,  
CC for stimulating the proliferation of or gene expression in pericyte  
CC cells, for stimulating the release of proteoglycans from cartilage, for  
CC stimulating the proliferation of inner ear utricular supporting cells,  
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating  
CC the release of a cytokine from PBMC cells, for inhibiting the binding of  
CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte  
CC cells, for stimulating proliferation of endothelial cells, for detecting  
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,  
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes  
CC are useful for isolating genomic and cDNA nucleotide sequences or  
CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful  
CC in assays to identify other proteins or molecules involved in binding  
CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome  
CC and gene mapping, in generation of antisense RNA and DNA, in the  
CC preparation of PRO polypeptide, for generating transgenic animals or  
CC knockout animals which in turn are useful in the development and  
CC screening of therapeutically useful reagents, in gene therapy, for  
CC chromosome identification, as chromosome marker, and for generating  
CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.  
CC detecting its expression in specific cells, tissues or serum, and for  
CC affinity purification of PRO from recombinant cell culture or natural  
CC sources. (I) and (II) are useful for tissue typing. This is the amino  
CC acid sequence of a novel human secreted and transmembrane PRO  
CC polypeptide.

XX

SQ Sequence 379 AA;

Query Match 99.6%; Score 1708; DB 6; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
Db 44 GDVDDAGDCSGARYNDWSDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 181  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 283

Qy 242 QVPSSLGSLSFNKKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
Db 284 QVPSSLGSLSFNKKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343

Qy 302 ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 337

Db 344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

RESULT 14

ADA76166

ID ADA76166 standard; protein; 379 AA.

XX

AC ADA76166;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human PRO polypeptide #108.

XX

KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;  
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;  
KW liver; microvascular endothelial cell; glucose; FFA;  
KW skeletal muscle cell; adipocyte cell; pericyte cell;  
KW inner ear utricular supporting cell; T-lymphocyte cell;  
KW endothelial cell tube formation; bone disorder; cartilage disorder;  
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;  
KW immune system cell infiltration.

XX

OS Homo sapiens.

XX

PN US2003073212-A1.

XX

PD 17-APR-2003.

XX

PF 16-APR-2002; 2002US-00123903.

XX

PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.

PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2003-687639/65.

DR N-PSDB; ADA76165.

XX

PT New isolated nucleic acid encoding a secreted and transmembrane  
PT polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and  
PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.

XX

PS Claim 12; Fig 216; 659pp; English.

XX

CC The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The  
CC polynucleotides are useful in molecular biology, including uses as  
CC hybridisation probes, in chromosome and gene mapping, in generating  
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also  
CC be used in preparing PRO polypeptides by recombinant techniques and in  
CC generating either transgenic animals or knock-out animals which are  
CC useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides or antibodies are used in preparing a  
CC medicament for treating a condition responsive to the polypeptides or  
CC antibodies, such as tumours, for stimulating and inhibiting proliferation  
CC of human microvascular endothelial cells, for modulating the uptake of  
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for  
CC stimulating differentiation of adipocyte cells, for stimulating  
CC proliferation of or gene expression in pericyte cells, for stimulating  
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte  
CC cells, for inducing endothelial cell tube formation and for treating

CC various bone and/or cartilage disorders such as sports injuries and  
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans  
CC from cartilage are useful for treating sports-related joint problems,  
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO  
CC polypeptides are also useful for treating various mammalian haemoglobin-  
CC associated disorders such as various thalassaemias and conditions which  
CC may benefit from enhanced local immune system cell infiltration. This  
CC sequence represents a human PRO polypeptide of the invention. Note: The  
CC sequence data for this patent is also available in electronic format from  
CC USPTO at seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 379 AA;

Query Match 99.6%; Score 1708; DB 6; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLNLAENPAMTRELLRA 241  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLNLAENPAMTRELLRA 283

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343

Qy 302 ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 337  
Db 344 ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 379

RESULT 15

ADA18816

ID ADA18816 standard; protein; 379 AA.

XX

AC ADA18816;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human PRO polypeptide #108.

XX

KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;  
KW colon; breast; prostate; rectum; cervix; liver; tumour; cancer;  
KW glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;  
KW cartilage; inner ear utricular supporting cell; cytokine; A-peptide;

KW factor VIIA; endothelial cell.  
XX  
OS Homo sapiens.  
XX  
PN US2003054517-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 08-MAY-2002; 2002US-00141755.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI; 2003-521854/49.  
DR N-PSDB; ADA18815.  
XX  
PT New PRO nucleic acid, useful for preparing a composition for treating  
PT e.g., tumors.  
XX  
PS Claim 12; Fig 216; 660pp; English.  
XX  
CC The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,  
CC prostate, rectal, cervical and liver tumours). The polynucleotides are  
CC useful in molecular biology, including uses as hybridisation probes, in  
CC chromosome and gene mapping, in generating antisense RNA and DNA and in  
CC gene therapy. The polynucleotides may also be used in preparing PRO  
CC polypeptides by recombinant techniques and in generating either  
CC transgenic animals or knock-out animals which are useful in the  
CC development and screening of therapeutically useful reagents. The PRO  
CC polypeptides or antibodies are used in preparing a medicament for  
CC treating a condition responsive to the polypeptides or antibodies, such  
CC as tumours, for modulating the uptake of glucose or FFA by adipocyte  
CC cells, for stimulating the proliferation of or gene expression in  
CC pericyte cells, for stimulating the release of proteoglycans from  
CC cartilage, for stimulating the proliferation of inner ear utricular  
CC supporting cells, for stimulating the release of cytokines from PBMC  
CC cells, for inhibiting the binding of A-peptide to factor VIIA, for  
CC inhibiting the differentiation of adipocyte cells and for stimulating the  
CC proliferation of endothelial cells. This sequence represents a human PRO  
CC polypeptide of the invention. Note: The sequence data for this patent is  
CC also available in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 379 AA;  
  
Query Match 99.6%; Score 1708; DB 6; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-162;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
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Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103  
  
Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
| ||| .||||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163  
  
Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 181  
| ||| .||||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 223  
  
Qy 182 GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqvlkllnlaenpamtrellra 241

Db            ||||||| 224 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 283

Qy            242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 301  
              |||||||

Db            284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 343

Qy            302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
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Db            344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

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Job time : 77.8455 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

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(without alignments)  
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1713	99.9	337	4	US-09-780-996A-9	Sequence 9, Appli
2	1708	99.6	379	3	US-09-193-266-1	Sequence 1, Appli
3	1708	99.6	379	4	US-10-140-002-216	Sequence 216, App
4	203.5	11.9	258	4	US-10-000-489-30	Sequence 30, Appl
5	176	10.3	59	4	US-09-513-999C-7259	Sequence 7259, Ap
6	109	6.4	536	4	US-09-248-796A-20705	Sequence 20705, A
7	100.5	5.9	561	4	US-09-270-767-42679	Sequence 42679, A
8	100.5	5.9	672	4	US-09-270-767-46165	Sequence 46165, A
9	100	5.8	402	2	US-08-290-731C-14	Sequence 14, Appl
10	100	5.8	704	4	US-09-248-796A-16001	Sequence 16001, A
11	100	5.8	911	3	US-09-356-952-6	Sequence 6, Appli

12	99.5	5.8	10182	3	US-09-134-001C-3159	Sequence 3159, Ap
13	97.5	5.7	5024	4	US-09-710-279-2964	Sequence 2964, Ap
14	97	5.7	812	4	US-09-538-092-643	Sequence 643, App
15	97	5.7	937	4	US-09-538-092-980	Sequence 980, App
16	96.5	5.6	265	4	US-09-248-796A-15824	Sequence 15824, A
17	96	5.6	682	3	US-08-982-785A-9	Sequence 9, Appli
18	96	5.6	682	4	US-09-629-498-9	Sequence 9, Appli
19	95	5.5	712	4	US-09-248-796A-19645	Sequence 19645, A
20	94	5.5	845	4	US-09-248-796A-15394	Sequence 15394, A
21	92.5	5.4	286	4	US-09-252-991A-23234	Sequence 23234, A
22	92.5	5.4	596	4	US-09-752-165-2	Sequence 2, Appli
23	92.5	5.4	732	4	US-09-614-912-24	Sequence 24, Appli
24	91.5	5.3	447	4	US-09-205-258-408	Sequence 408, App
25	91.5	5.3	461	4	US-10-140-002-454	Sequence 454, App
26	91	5.3	229	4	US-09-710-279-992	Sequence 992, App
27	91	5.3	243	3	US-09-134-001C-3587	Sequence 3587, Ap
28	91	5.3	560	2	US-08-643-034A-2	Sequence 2, Appli
29	91	5.3	560	3	US-08-648-650A-2	Sequence 2, Appli
30	91	5.3	560	3	US-09-183-266A-2	Sequence 2, Appli
31	90.5	5.3	1279	4	US-09-710-279-3188	Sequence 3188, Ap
32	90.5	5.3	3696	3	US-09-134-001C-5080	Sequence 5080, Ap
33	89.5	5.2	251	4	US-09-248-796A-14669	Sequence 14669, A
34	89.5	5.2	388	4	US-09-134-000C-5878	Sequence 5878, Ap
35	89.5	5.2	546	4	US-09-907-794A-250	Sequence 250, App
36	89.5	5.2	546	4	US-09-905-125A-250	Sequence 250, App
37	89.5	5.2	546	4	US-09-902-775A-250	Sequence 250, App
38	89.5	5.2	546	4	US-09-906-700-250	Sequence 250, App
39	89.5	5.2	546	4	US-09-903-603A-250	Sequence 250, App
40	89.5	5.2	666	3	US-08-982-785A-11	Sequence 11, Appli
41	89.5	5.2	666	4	US-09-629-498-11	Sequence 11, Appli
42	89.5	5.2	780	4	US-09-198-452A-920	Sequence 920, App
43	89.5	5.2	2954	4	US-09-150-867-1	Sequence 1, Appli
44	88.5	5.2	453	4	US-09-328-352-4242	Sequence 4242, Ap
45	88.5	5.2	465	4	US-09-248-796A-19538	Sequence 19538, A

## ALIGNMENTS

RESULT 1  
 US-09-780-996A-9  
 ; Sequence 9, Application US/09780996A  
 ; Patent No. 6696273  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maury, Isabella  
 ; APPLICANT: Mercken, Luc  
 ; APPLICANT: Fournier, Alain  
 ; TITLE OF INVENTION: Partners of the PTB1 Domain of FE65, Preparation and Uses  
 ; FILE REFERENCE: ST00004-US  
 ; CURRENT APPLICATION NUMBER: US/09/780,996A  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: FR00/01628  
 ; PRIOR FILING DATE: 2000-02-10  
 ; PRIOR APPLICATION NUMBER: US 60/198,500  
 ; PRIOR FILING DATE: 2000-04-18  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 9
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: X=G, D, V, or A
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (305)..(305)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-780-996A-9
```

## RESULT 2

US-09-193-266-1

```
; Sequence 1, Application US/09193266
; Patent No. 6214582
; GENERAL INFORMATION:
; APPLICANT: Marcu, Kenneth B.
; TITLE OF INVENTION: Y2H35 A Strong IKK Binding Protein
; FILE REFERENCE: 178-257
; CURRENT APPLICATION NUMBER: US/09/193,266
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 379
; TYPE: PRT
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; ORGANISM: Homo sapiens  
US-09-193-266-1

Query Match 99.6%; Score 1708; DB 3; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-175;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
|||  
Db 44 GDVDDAGDCSGARYNDWSDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103  
  
Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
|||  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163  
  
Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
|||  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223  
  
Qy 182 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
|||  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA 283  
  
Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 301  
|||  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 343  
  
Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
|||  
Db 344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

RESULT 3

US-10-140-002-216

; Sequence 216, Application US/10140002

; Patent No. 6725730

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C59

; CURRENT APPLICATION NUMBER: US/10/140,002  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 216  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-140-002-216

Query Match 99.6%; Score 1708; DB 4; Length 379;  
Best Local Similarity 99.7%; Pred. No. 8.3e-175;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 61  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrelra 241  
Db 224 GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrelra 283

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 301  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 343

Qy 302 ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 337  
Db 344 ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 379

RESULT 4

US-10-000-489-30  
; Sequence 30, Application US/10000489  
; Patent No. 6794363  
; GENERAL INFORMATION:  
; APPLICANT: Benjanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US6.DIV  
; CURRENT APPLICATION NUMBER: US/10/000,489  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277

; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: JPatent  
; SEQ ID NO 30  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
; NAME/KEY: UNSURE  
; LOCATION: 49  
; OTHER INFORMATION: Xaa = Glu, \*  
US-10-000-489-30

Query Match 11.9%; Score 203.5; DB 4; Length 258;  
Best Local Similarity 46.5%; Pred. No. 2e-13;  
Matches 47; Conservative 19; Mismatches 22; Indels 13; Gaps 3;  
  
QY 39 RIGTEAGTRA---RARARARATRA-----RRAVQKRASPNSDDTVLSPQELQKVLC 87  
| |: || || : :||::||| || | | | :|| :|||| :  
Db 156 RSGSRAGGRASGKSKGKARSKSTRAPATTWPVRRG--KFNFPYKIDDILSAPDLQKVLC 213  
  
QY 88 VEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGPLIVAK 128  
:| : |:|| |: |||||||:||:: ||:|||:||:|||  
Db 214 LERTNDPFIQEVALVTLGNNAAYSFNQNAIRELGGVPIIAK 254

## RESULT 5

US-09-513-999C-7259  
; Sequence 7259, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 7259  
; LENGTH: 59  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-7259

Query Match 10.3%; Score 176; DB 4; Length 59;  
Best Local Similarity 58.9%; Pred. No. 1.8e-11;

Matches 33; Conservative 12; Mismatches 11; Indels 0; Gaps 0;  
Qy 222 LKLLNLAEVPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWE 277  
Db :||::| |||||||||: :||| | ||||: ::||:| :| :||||||| ||  
1 MKLIINFTENPAMTRELVSCKVPSLISLFNKEWDREILLNILTGFENINDNIKNE 56

RESULT 6

US-09-248-796A-20705  
; Sequence 20705, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 20705  
; LENGTH: 536  
; TYPE: PRT  
; ORGANISM: Candida albicans  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (123)  
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown.

US-09-248-796A-20705

Query Match 6.4%; Score 109; DB 4; Length 536;  
Best Local Similarity 25.0%; Pred. No. 0.0088;  
Matches 65; Conservative 35; Mismatches 84; Indels 76; Gaps 14;

Qy 116 IIRDLGGL-PIVAKILNTRDPIVKEKALIVLNNLSVNAEN-QRRLKVYMNQVCDDT--IT 171  
Db 243 LINDVEGISEIVLECLNDRDLIIRKALEVSNYL-VNEDNITEVVVKIMLMQLVPDNNMID 301

Qy 172 SRLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFRFLFSAGNEETKLQVLKLLLNL-- 228  
Db 302 DMLKLEITLKILQIASQNNYVN----IPN----FRWYVA-----VLKDVINLTLL 343

Qy 229 ----AENPAMTRELLRAQVPSSLGSLFNKKENK--EVILKLL--VIFENIND----- 272  
Db 344 PVEGATNSGLIASHIANEISTEVGKEFKNLATKVPNSVRSYLLQNVVLELVQDVRLLDSSA 403

Qy 273 ----NFKW-----EENEPTQNQFGE-----SLFFFLKEFQV 300  
Db 404 LILKDLYWILGEYISELKVTQNDDGDDSDSDGEDAQVMVLIDKKIKVFNTLINYQI 463

Qy 301 CADKXLGIESHHDFLVKVKV 320  
|| ||: |: | | |:



; ORGANISM: Drosophila melanogaster  
US-09-270-767-46165

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Query Match           5.9%; Score 100.5; DB 4; Length 672;
Best Local Similarity 22.1%; Pred. No. 0.1;
Matches 46; Conservative 29; Mismatches 94; Indels 39; Gaps 4;

    78 PQELQKVLCLVEMSEKPYILEAAIALGNNAAYAFN----RDIIRD LGGLPIVAKILNT 132
        | : | | | :: | | |||| | : | : | : | : | ||| : :: |
326 PEVVQYYLSLLQSCSNPETLEAAAGAIQNLSACYWQPSIDIRATVRKEKGLPILVELLRM 385

    133 RDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLLTNMTVT 192
        | | | ||::: | : : | | | : | | : | | : | | : | | : | | : | | : |
386 EVDRVVCAVATALRNLAIDQRNKELIGKY-----AMRDLVQKLPS 425

    193 NEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNL AENPAMTRELLRAQVPSSLGSLFN 252
        || | | : : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
426 GNVQHDQNTSDDTTAVLATINEVIK-----KNPEFSSRLLDS---GGIDRLMN 471

    253 KK ENKEVILKLLVIFENINDNFKWEENE 280
        : | | | : | : | : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
472 ITKRKEKYTSCVLKFASQVLYTMWQHNE 499

```

### RESULT 9

US-08-290-731C-14

; Sequence 14, Application US/08290731C

; Patent No. 5843646

**GENERAL INFORMATION:**

; APPLICANT: BOWTELL, David Douglas Lawrence  
; TITLE OF INVENTION: DNA MOLECULES ENCODING MURINE  
; TITLE OF INVENTION: SON OF SEVENLESS (mSOS) GENE,  
; TITLE OF INVENTION: AND mSOS POLYPEPTIDES  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:

; CORRESPONDENCE ADDRESS:  
ADDRESSEE SIGNATURE

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 PENNSYLVANIA AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

**CURRENT APPLICATION DATA:**

APPLICATION NUMBER: US/08/290,731C

FILING DATE: 17-OCT-1994

CLASSIFICATION: 435

**CLASSIFICATION: 100**

**APPLICATION NUMBER:**

FILING DATE: 17-FEB-1993

FILED DATE: 17-FEB-1993  
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

APPLICATION NUMBER: PL0921/92  
FILING DATE: 13 FEB 1992

FILING DATE: 17-FEB-1992  
ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon  
REGISTRATION NUMBER: 30,764  
REFERENCE/DOCKET NUMBER: Q-36066  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 402 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-290-731C-14

Query Match 5.8%; Score 100; DB 2; Length 402;  
Best Local Similarity 22.9%; Pred. No. 0.052;  
Matches 62; Conservative 36; Mismatches 77; Indels 96; Gaps 14;

Qy 70 NSDDTV-----LSPQELQKVLCVEMSEKPYILEAALIALGNNAAYAFNRDIIRDL 120  
|| | : | | : | : | || : | : |  
Db 155 NSPDPIIYKDELVILLPPREIAKOLCILEFOSFSHI----- 190

Qy 121 GGLPIVAKI---LNTRDPIVKEK-ALIVLNNL SVN-----AENQRRLKV--YMNOV 165  
.....::||| || | ||| : ||:||| | :|||

Db 191 SRIQFLTKIWIDELNRFSP--KEKTSTFYLSNHLVNFTETIVQEEEPRRTNVLAYFIQV 248

Qy 166 CD-----DTITSRLNS-----SVQLAGLRLLTNMTVT---NEYQ 196  
|| :| || || | | || :| :|

DB 249 CDYLRELNNFASLFSIISALNNSPIHRLRKTWANLNSTKLASFELLNLTEARKNFSNYR 308

309 DCEENCVEPCVPPFLGVYFTD-LTFERKIGNKRDN---FQNMINFDRKTRVTRIENEIKRFQ 363

320 SVENSKA VÄG- OCH VATTENBYGGNING 331

## RESULT 10

US-09-248-796A-16001

; Sequence 16001, Application US/09248796A

; Patent No. 6747137

**; GENERAL INFORMATION:**

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

**TITLE OF INVENTION:** FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PBTOR APPLICATION NUMBER: US

PRIORITY FILING DATE: 1998-02-13

PRIOR FILING DATE: 1990-02-13  
PRIORITY APPLICATION NUMBER: US 60/096 409

PRIOR REFLECTION NUMBER: 05  
PRIOR FILING DATE: 1998-08-13

PRICK FILING DATE: 1990-06-15  
NUMBER OF SEQ ID NOS: 28208

, NUMBER OF SEQ ID NOS: 20200

; SEQ ID NO 16001  
; LENGTH: 704  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-16001

Query Match 5.8%; Score 100; DB 4; Length 704;  
Best Local Similarity 21.1%; Pred. No. 0.12;  
Matches 52; Conservative 55; Mismatches 96; Indels 44; Gaps 13;

Qy 74 TVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRD----LGGLPIVAK 128  
Db 239 TVLS-EEAQ--LCL--KPEPGLLIRAMAISIDN--PESFDVVVVRGFFDMLSHIPLDSD 291

Qy 129 ILNTR-DPIVKEKALIVLNNSVNAEN--QRRLKVMNQVCDDTITSRLNSSVQLAGLRL 185  
Db 292 VITNRITPTDREVLIMACSKITLRKDMSLNRRLWTYF-----LGPETEHESLKA 340

Qy 186 LTNMTVTNEY--QHMLANSISDFRFLFSAGNEETKLQVLKLLLNAENPAMTRELLRAQV 243  
Db 341 LTR---TEYFKQYVEETLINGLLAMAHSKIELKCDAFKILLPLIMDKWEIGNVLTPKL 396

Qy 244 PSS-LGSLFNKKENKEVILKLLVIFENINDNFKW-----EENEPTQNQFGEGLFF 293  
Db 397 FSSFLKIAYNNDHQDLMISASTLFDGVESIYIWSDIIGVILSDESDEEEHEF--DVVFH 454

Qy 294 FLKEFQV 300  
Db 455 VLKDFNV 461

RESULT 11  
US-09-356-952-6  
; Sequence 6, Application US/09356952  
; Patent No. 6117663  
; GENERAL INFORMATION:  
; APPLICANT: Boriack-Sjodin, Ann  
; APPLICANT: Margarit, S. M.  
; APPLICANT: Bor-Sogi, Dafna  
; APPLICANT: Cole, Philip  
; APPLICANT: Kuriyan, John  
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 600-1-228N  
; CURRENT APPLICATION NUMBER: US/09/356,952  
; CURRENT FILING DATE: 1999-07-19  
; EARLIER APPLICATION NUMBER: 60/093,631  
; EARLIER FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 911  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-09-356-952-6

Query Match 5.8%; Score 100; DB 3; Length 911;

Best Local Similarity 22.98; Pred. No. 0.19;  
Matches 62; Conservative 36; Mismatches 77; Indels 96; Gaps 14;

RESULT 12

US-09-134-001C-3159

; Sequence 3159, Application US/09134001C

Patent No. 6380370

**GENERAL INFORMATION:**

: APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; STAPHYLOCOCCUS

**TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS**

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/08/134 001C

CURRENT APPLICATION NUMBER: US/01-10000  
CURRENT FILING DATE: 1998-08-13

BRIEF APPLICATION NUMBER: US 60/064 861

PRIOR APPLICATION NUMBER: 03  
PRIOR FILING DATE: 1997.11.08

PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US

PRIOR APPLICATION NUMBER: US 60/055,779

; PRIORITY FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5634

; NUMBER OF SEQ ID NOS: 36/4  
; SEQ ID NO: 3150

; LENGTH: 10192

; LENGTH: 10182

; TYPE: PRT  
ORGANISM: *S. cerevisiae*

; ORGANISM: Staph

Query Match 5.8%; Score 99.5; DB 3; Length 10182;  
Best Local Similarity 21.7%; Pred. No. 8.8;  
Matches 53; Conservative 54; Mismatches 104; Indels 33; Gaps 8;

```

Qy      58  RARRAVQKRASPNSDDTVLSPQELQKVLCLEMSEKPYILEAAALIALGNNAAYAFN---- 113
       | :: : : ::|      ::| |:::   |::|: | | | |: :|| |
Db      7876 RVVKQIINQTSNP----TMNPLEVERATSNVKISKDALHGERELNDKNNSKTFAVNHLDN 7930

Qy      114 -----RDIIRDLGGLPIVAKILNTRDPIVKEKAL---IVLNNLSVNAENQRRLKVYMN 163
       : :: | |::: | : | || || | : : | : | : |:

```

Db 7931 LNQAQKEALTHEIEQATIVSQVNNIYN---KAKALNNDMKKLKDIVAQQDNVRQSNNYIN 7987  
Qy 164 QVCDDTITSRLNSSVQLAG--LRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQV 221  
: | | : | :: | : : | |::: : |:|: : | : | |||  
Db 7988 E--DSTPQNMYNDTINHAQSIIDQVANPTMSHD---EIENAINNIKHAINALDGEHKLQQ 8042  
Qy 222 LKLLLNLAENPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEP 281  
| | | : | | :: | |: : | : : | : : || | | | |  
Db 8043 AKENANLLIN--SLNDLNAPQRDAINRLVNEAQTREKVAEQLQSAQALNDAMKHLRNS- 8098  
Qy 282 TQNQ 285  
|||  
Db 8099 IQNQ 8102

## RESULT 13

US-09-710-279-2964  
; Sequence 2964, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2964  
; LENGTH: 5024  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5024)  
; OTHER INFORMATION: variable amino acid  
US-09-710-279-2964

Query Match 5.7%; Score 97.5; DB 4; Length 5024;  
Best Local Similarity 21.7%; Pred. No. 4.8;  
Matches 53; Conservative 53; Mismatches 105; Indels 33; Gaps 9;

Qy 58 RARRAVQKRASPNSDDTVLSPQELQVKVLCLVEMSEKPYILEAAALIALGNNAAYAFN---- 113  
| :: : : : | :: | : :: | : | : | | | : | |  
Db 2930 RVKQIINQTSNP-----TMNPLEVERATSNVKTSKDALHGERELNDKNSKTFAVNHLN 2984  
Qy 114 -----RDIIRD LGGLPIVAKILNTRDPIVKEKAL---IVLNNLSVNAENQRRLK VYMN 163  
: :: | |::: | : | | | | : : | : | : | : |  
Db 2985 LNQAQKEALTHEIEQATIVSQVNNIYN---KAKALNNDMKKLKDIVAQQDNVRQSNNYIN 3041  
Qy 164 QVCDDTITSRLNSSVQLAG--LRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQV 221  
: | | : | :: | : : | |::: : |:|: : | : | |||  
Db 3042 E--DSTPQNMYNDTINHAQSIIDQVANPTMSHD---EIENAINNIKHAINALDGEHKLQQ 3096



Qy	243 ---VPSSLGSLFNK-----KENKEVILKLLVIFENINDNFK-----WEENEPT 282 :   :     :         :   :: :  ::
Db	297 LTLLIPSRFDASANLSYQPIDQWKSSFNDISKLLSILDQTIDTYQVNEFADPIDFIEDEPK 356
Qy	283 QNQFGE---GSLFFFHK---EFQVCADKXLGIESH-HDFLVVK 319 ::     :   ::        :    :: :::
Db	357 EDSDGVKRILGSIFSFSVERLDEFM--KSLLNIDPHSSDYLIRLR 399

RESULT 15

US-09-538-092-980

; Sequence 980, Application US/09538092

; Patent No. 6753314

**; GENERAL INFORMATION:**

; APPLICANT: Giot, Loic

; APPLICANT: Mansfield, Traci A.

; TITLE OF INVENTION: Prote

; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/0

; CURRENT FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: 60/

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/1  
1234567890123456789012345678901

; PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEC. IP. NO. 1267

; NUMBER OF SEQ ID NOS: 1387

; SOFTWARE: CuraPatSeqFormatter Version 0.9  
SEQ\_ID\_NG\_880

; SEQ ID NO 980  
; LENGTH: 937

; LENGTH: 937

; TYPE: PRI  
; ORGANISM:

; ORGANISM: *Homo sapiens*  
; FEATURE:

**FEATURE:  
NAME/KEY**

NAME/REF: RESC\_read  
LOCATION: (0) - (0)

OTHER INFORMATION: Poly

US-09-538-092-980

85 85 558 892 588

Query Match 5.7% Score 97% DB 4% L

Best Local Similarity 19.8%; Pred. No. 0.41;  
Matches 44; Conservative 46; Mismatches 74; Indels 58; Gaps 10;

Qy 86 CLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKALIVL 145  
|| : | ||: : | : : | : | : | | | : : | : | : | | |

Qy 170 ITSRL---NSSVQLAGLRLLTN----MTVTNEYQHMLANSISDFFRLFSAGNEETKLQLV 222  
  :| || | ||:| | :| :|| | :| :| | :| | :| |

Qy 223 K-LLLNLAENPAMTRELLRAQPSSLGSLFNKKENKEVILKL

Search completed: January 7, 2005, 14:51:42  
Job time : 23.1064 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2005, 14:33:20 ; Search time 17.1939 Seconds  
(without alignments)  
1885.849 Million cell updates/sec

Title: US-10-726-721A-9

Perfect score: 1715

Sequence: 1 RGDVDDAGDCSGARYNDWSD.....VKVGKFMALKLAEHMFPKSQE 337

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	781.5	45.6	453	2	JC7582	armadillo (arm) rep
2	683	39.8	632	2	T00084	hypothetical prote...
3	345	20.1	1395	2	T00068	hypothetical prote
4	127.5	7.4	744	2	A32905	plakoglobin, desmo
5	117.5	6.9	578	2	S50446	VAC8 protein - yea
6	112	6.5	630	2	G87753	protein C43E11.8 [
7	109	6.4	619	2	A36682	72K mitochondrial
8	108.5	6.3	867	2	B96625	hypothetical prote
9	107.5	6.3	876	2	T51951	gamma-adaptin 1 [i
10	107	6.2	629	2	B64075	transcription init
11	106.5	6.2	580	2	F84471	hypothetical prote
12	106.5	6.2	729	2	A86416	probable arm repea
13	105	6.1	428	2	T27763	hypothetical prote

14	104	6.1	464	2	S50541	hypothetical prote
15	104	6.1	1830	2	E82909	conserved hypothet
16	103	6.0	449	2	T26571	hypothetical prote
17	103	6.0	993	2	A96750	hypothetical prote
18	103	6.0	1387	2	T16511	hypothetical prote
19	101	5.9	711	2	F86373	protein T23E23.12
20	101	5.9	1299	2	A86366	T26J12.6 protein -
21	100.5	5.9	251	2	G75063	hypothetical prote
22	100.5	5.9	476	2	T52157	hypothetical prote
23	100.5	5.9	1979	2	C71622	hypothetical prote
24	100	5.8	888	2	A38539	p101 protein precu
25	100	5.8	895	2	T11979	Preprotein translo
26	100	5.8	911	2	S28098	guanine-nucleotide
27	100	5.8	1802	2	G71616	hypothetical prote
28	99.5	5.8	1046	2	A86790	ATP-dependent dsDN
29	99	5.8	2048	2	C84609	hypothetical prote
30	99	5.8	3066	1	JQ1662	genome polyprotein
31	97.5	5.7	459	2	T39473	probable geranylge
32	97.5	5.7	949	2	D97781	hypothetical prote
33	97.5	5.7	1164	2	T24806	hypothetical prote
34	97	5.7	522	2	A57319	overgrown hematopo
35	97	5.7	618	2	D86364	hypothetical prote
36	97	5.7	924	2	T00518	hypothetical prote
37	97	5.7	937	2	A35553	beta-adaptin - hum
38	97	5.7	937	2	C35553	beta-adaptin - rat
39	96.5	5.6	253	2	B71168	hypothetical prote
40	96.5	5.6	738	2	S35093	plakoglobin - Afri
41	96	5.6	966	2	D96662	hypothetical prote
42	95.5	5.6	868	2	AE1953	hypothetical prote
43	95	5.5	372	2	C83766	adenine glycosylas
44	95	5.5	511	2	E90600	hypothetical prote
45	95	5.5	865	2	T41685	probable gamma-ada

## ALIGNMENTS

### RESULT 1

JC7582

armadillo(arm) repeat protein ALEX1 - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004

C;Accession: JC7582

R;Kurochkin, I.V.; Yonemitsu, N.; Funahashi, S.; Nomura, H.

Biochem. Biophys. Res. Commun. 280, 340-347, 2001

A;Title: ALEX1, a novel human armadillo repeat protein that is expressed differentially in normal tissues and carcinomas.

A;Reference number: JC7582; MUID: 21092608; PMID:11162520

A;Accession: JC7582

A;Molecule type: mRNA

A;Residues: 1-453 <KUR>

A;Cross-references: UNIPROT:Q9P291; DDBJ:AB039670

C;Comment: This protein is involved in regulation of normal cell growth, cell-to-cell signaling or in establishment of cell polarity, and such plays a role in tumor suppression.

C;Genetics:

A;Gene: alex1

A;Map position: Xq21.33-q22.2

C;Keywords: tandem repeat; transmembrane protein

Query Match 45.6%; Score 781.5; DB 2; Length 453;  
Best Local Similarity 52.3%; Pred. No. 1.4e-49;  
Matches 157; Conservative 56; Mismatches 74; Indels 13; Gaps 3;

Qy 39 RIGTEAGTRA---RARARARATRA-----RRAVQKRASPNSDDTVLSPQELQKVLC 87  
| | : || || : : || :: || || || | | : || : || || :  
Db 156 RSGSRAGGRASGKSKGKARSKSTRAPATTWPVRRG--KFNFPYKIDDILSAPDLQKVLCI 213

Qy 88 VEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGPLIVAKILNTRDPIVKEKALIVLNN 147  
: | : | : || : || || || : || : || : || : || : || : || : || : || : ||  
Db 214 LERTNDPFIQEVALVTLGNNAAYSFNQNAIRELGGVIIAKLIKTKDPIIREKTYNALNN 273

Qy 148 LSVNAENQRRLKVMNQVCDDTITSRLNSSVQLAGRLLLTNMTVTNEYQHMLANSISDFF 207  
|||||| || : | : || || : || : || : || || || || || || || : | || ||  
Db 274 LSVNAENQGKIKTYISQVCDDTMVCRLDSAVQMAGLRLLTNMTVTNHYQHLLSYSFPDFF 333

Qy 208 RLFSAGNEETKLQLKLLLNLAEVPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIF 267  
| | || | : || : || : || || || || : || | || || : : || : | : ||  
Db 334 ALLFLGNHFTKIQIMKLIINFTEVPAMTRELVSCKVPSLISLFNKEWDREILLNILT 393

Qy 268 ENINDNFKWEENEPTQNQFGEGLFFFKEFQVCADKXLGIESHHDFLVVKVKVGKFMAKL 327  
|||||| | | : : | || || || || | : : || : || || | : ||  
Db 394 ENINDNIKNEGGLASSRKEFSRSSLFFLFKESGVCVKKIKALANHNDLVVKVLKVLTKL 453

## RESULT 2

T00084

hypothetical protein KIAA0512 - human

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 09-Jul-2004

C;Accession: T00084

R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.

DNA Res. 5, 31-39, 1998

A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.

A;Reference number: Z14086; MUID:98290545; PMID:9628581

A;Accession: T00084

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-632 <NAG>

A;Cross-references: UNIPROT:O60267; EMBL:AB011084; NID:g3043547;..

PIDN:BAA25438.1; PID:g3043548

A;Experimental source: brain; clone HF0239

C;Genetics:

A;Note: KIAA0512

Query Match 39.8%; Score 683; DB 2; Length 632;  
Best Local Similarity 45.3%; Pred. No. 3.4e-42;  
Matches 140; Conservative 56; Mismatches 91; Indels 22; Gaps 3;

Qy 18 WSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARRAVQKRASPNSDDTVLS 77  
| : | : || : | : | | | | : || | | : | : |

Db 345 WTDTESDSD-----SEPETQRRGRGRRPV----AMQKRPFPYEIDEILG 384  
 Qy 78 PQELQKVLCVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGLPIVAKILNTRDPV 137  
     ::|:|| |:: | : |: | : ||: | ||| |: |:: | || |||||:| ::| || :  
 Db 385 VRDLRKVLALLQKSDDPFIQQVALTLSNNANYSNCQETIRKLGGLPIIANMINKTDPHI 444  
 Qy 138 KEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQH 197  
     |||||: :|||| | ||| ||:||||:| || : | |||:||: ||: |||||:||:|||  
 Db 445 KEKALMAMNNLSENYENQGRLQVYMNKVMDDIMASNLSAVQVVGLKFLTNMTITNDYQH 504  
 Qy 198 MLANSISDFRFLFSAGNEETKLQVLKLLNLAEAPAMTRELLRAQVPSSLGSLFNKKENK 257  
     :| |||:|||| | | : |:::||:| | |||| | :|| | |||:| ||:|  
 Db 505 LLVNSIANFFRLLSQGGGKIKVEILKILSNFAENPDMLKKLLSTQVPASFSSLNSYVES 564  
 Qy 258 EVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVCADKXLGIESHHDFLVK 317  
     |::: | :|| | || :| :| :||||: | || | : :||| |||  
 Db 565 EILINALTLFEIIYDNLRAEVF--NYREFNKGSLFYLCTTSGVCVKIRALANHHDLLVK 622  
 Qy 318 VKVGKFMAK 326  
     ||| | : |  
 Db 623 VKVIKLVNK 631

### RESULT 3

T00068

hypothetical protein KIAA0443 - human

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 09-Jul-2004

C;Accession: T00068

R;Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.  
DNA Res. 4, 307-313, 1997

A;Title: Prediction of the coding sequences of unidentified human genes. VIII. 78 new cDNA clones from brain which code for large proteins in vitro.

A;Reference number: Z14084; MUID:98116655; PMID:9455477

A;Accession: T00068

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1395 <ISH>

A;Cross-references: UNIPROT:O43168; EMBL:AB007903; NID:d1175359;

PIDN:BAA23715.1; PID:d1024620

A;Experimental source: brain; clone HJ0137

C;Genetics:

A;Note: KIAA0443

Query Match 20.18; Score 345; DB 2; Length 1395;  
 Best Local Similarity 36.1%; Pred. No. 4.7e-17;  
 Matches 73; Conservative 49; Mismatches 80; Indels 0; Gaps 0;

Qy 76 LSPQELQKVLCVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGLPIVAKILNTRDP 135  
     : :| ::| |:| |:| | : ||:| :| | || ||| | : :: :||  
 Db 1151 IGSEEFELLMEKIRDPEFIHEISKIAMGMRSASQFTRDFIRDSGVVSLIETLLNYPSS 1210  
 Qy 136 IVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEY 195  
     |: | : : | : : | : ||:||:| : :| | ||:|:| : :| | :|  
 Db 1211 RVRTSFLENMIRMAPYPNLNIQTYICKVCEETLAYSVDSPEQLSGIRMIRHLTTTDY 1270

Qy	196 QHMLANSISDFRFLFSAGNEETKLQLKLLLNLAEAPMTRELLRAQVPSLGSLFNKKE 255 ::   :      :   : :    :    :    :     :        :
Db	1271 HTLVANYMSGFLSLLATGNAKTRFHVLKMLLNLSENLFMTKELLSAEAVSEFIGLFNREE 1330
Qy	256 NKEVILKLLVIFENINDNFKWE 277 :   :       :
Db	1331 TNDNIOIVLAIHENIGNNIKKE 1352

## RESULT 4

A32905

### plakoglobin, desmosomal - human

C; Species: *Homo sapiens* (man)

C;Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text change 09-Jul-2004

C;Accession: A32905

R; Franke, W.W.; Goldschmidt, M.D.; Zimbelmann, R.; Mueller, H.M.; Schiller, D.L.; Cowin, B.

Proc. Natl. Acad. Sci. U.S.A. 86, 4027-4031, 1989

A:Title: Molecular cloning and amino acid sequence

A: Reference number: A32905; MUIID: 89264555; PMID: 2726765

A:REFERENCE NUMBER: A32905; A31B.89284595; THIB.2726765  
A:ACCESSION: A32905

A:Accession #: A92965  
A:Status: preliminary

## A. status: preliminary B. Molecules, tumors, mRNA

A;Molecule type: mRNA  
A;Residue no.: 1-344 (EBNA)

A;Residues: 1-744 <FRAG>  
A:Glycolic acid domain UNIT

A;Cross-references: UNIPROT:P14923; GB:M23410

## C; Genetics:

A;Gene: GDB:JUP

A;Cross-references: GDB:126565; OMIM:173325

A;Map position: 7pter-7qter

C;Keywords: cytoskeleton

Best Local Similarity 19.9%; Pred. No. 0.16;  
Matches 77; Conservative 49; Mismatches 122; Indels 139; Gaps 10;

Qy 54 ARATRARRAVQKRASPNSDDTVLSPQELQKVLCVEMSEKPYILEAALIALGNNAAYAFN 113  
           ||| | | | : | | : | : | : | | : | : | : | : | | | : | : | : | : | :  
 Db 80 ARAKRVREAMCPGVSGEGQLALLATQVEGQATNLQRLLAEPSQLLKSIAIVHLIN--YQDD 136

Qy 114 RDIIRDLGGGLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLK-----VYMNQ 164  
      :::     || : |:||    ||:| || ::::| ||    :::| |            | |  
Pb 137 AELVY TRAILETKILNDEPPIADATKAMVLYNQI SKKEASPPALMGSPLVAVADPTMO 194

Qy 165 VCDDTITSRLNSSV----- 178  
.. | | :| :|:  
.....

Qy 179 -----QLAGLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKL----- 219

Qy 220 -----QVLKLLLNLAE-----PAMTR-----ELLRAQVP----- 244

Db 315 VQIMRNYSYEKLLWTTSRVLKVLSVCPNSNKPAIVEAGGMQALGKHLSNSPRLVQNCLWT 374  
Qu 345 SSISSLNKKENKEVILKLIV LEEPNINDNEKTEENEPPTONEG 387

Db	375 LRNLSDVATKQEGLESVLKILVNQLSVDDNVNLTCAATGTLNSNLTNNSKNKTQNSGV 434
Qy	288 EGSLFFFKL-----EFQVCADKXL 306
Db	435 EALIHAILRAGDKDDITEPAVCALRHL 461

RESULT 5

S50446

VAC8 protein - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein YEL013w

C;Species: *Saccharomyces cerevisiae*

C;Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S50446

R;Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A;Description: *Saccharomyces cerevisiae* chromosome V cosmids 9871, 8199, 9867, 9495 and lambda clones 6693 and 5898.

A;Reference number: S50428

A;Accession: S50446

A;Molecule type: DNA

A;Residues: 1-578 <DIE>

A;Cross-references: UNIPROT:P39968; EMBL:U18530; NID:g602367; PID:g602380; GSPDB:GN00005; MIPS:YEL013w

C;Genetics:

A;Gene: SGD:VAC8; MIPS:YEL013w

A;Cross-references: SGD:S0000739; MIPS:YEL013w

A;Map position: 5L

C;Function:

A;Description: required for vacuole inheritance and protein targeting from the cytoplasm to vacuole

C;Keywords: yeast vacuole

Query Match 6.9%; Score 117.5; DB 2; Length 578;  
 Best Local Similarity 24.2%; Pred. No. 0.63;  
 Matches 59; Conservative 44; Mismatches 88; Indels 53; Gaps 9;

Qy	76 LSPQELQKVLCVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGL-PIVAKI----- 129
	:  : :  ::  : :  :               :  :  ::     ::  ::
Db	82 VSREVLEPILILLQ-SQDPQIQVAACAALGNLAVNNENKLLIVEMGGLEPLINQMMGDNV 140

Qy	130 -----LNTRD-----PI-----VKEKALIVLNNLSVNAEN 154
	:       :  :       :  :       :       :       :
Db	141 EVQCNAVGCITNLATRDDNKHKIATSGALIPLTKLAKSKHIRVQRNATGALLNMTHSEEN 200

Qy	155 QRRLKVYMNQVCDDTITSRLNSS---VQLAGLRLLTNMTVTNEYQHMLANS---ISdff 207
	::  :  :     :  :   :       :       :       :       :       :
Db	201 RKEL---VNAGAVPVLVSSLSSSTDPMVQYYCTTALSNIAVDEANRKLAQTEPRLVSKLV 257

Qy	208 RLFSAGNEETKLQVLKLLNLAENPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIF 267
	:  :           :  :
Db	258 SLMDSPSSRVKCQATLALRNLASDTSYQLEIVRAGGLPHLVKLI-QSDSIPLVLASVACI 316

Qy	268 ENIN 271
	:
Db	317 RNIS 320

RESULT 6

G87753

protein C43E11.8 [imported] - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C;Accession: G87753

R;anonymous, The *C. elegans* Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology.

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/ for a list of authors

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 285, 1493, 1999

A;Accession: G87753

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-630 <STO>

A;Cross-references: UNIPROT:P91149; GB:chr\_I; PIDN:AAB37623.1; PID:g1703569; GSPDB:GN00019; CESP:C43E11.8

C;Genetics:

A;Gene: C43E11.8

A;Map position: 1

Query Match 6.5%; Score 112; DB 2; Length 630;  
Best Local Similarity 22.6%; Pred. No. 1.8;  
Matches 78; Conservative 54; Mismatches 109; Indels 104; Gaps 18;

Qy	43 EAGTRARARAR-ATRARRAVQKRASPNSDDTVLSPQELQKVLC-----LVE     :: : :: :   :   :        : :   :  :     :	96
Db	248 EAQKSSQLASRSKLSTAVRKPVQR--SEKVD--VLIDLDACHAMCSALLS LEEK--L	301
Qy	97 LEAALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKALIVL----- :  :   :   :  :    : :  :       : ::	145
Db	302 MVKAIPDTSKRA-----QVFRELVSRLPLAYAVVQTQ-KVVNEKD DIGIVPLLPLHLLSQ	354
Qy	146 -----NNLSVNA-----ENQRLKV---YMNQVCDD-----TITS :  :  :   :  :    :	172
Db	355 NYARFHNLATNSIGDVQFDLSMRQLQVKCSSYVNEVIENLN EDTTKFVPPDGNVHPTTAS	414
Qy	173 RLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFFRFLFSAG NEETKLQVLKLLNLAENP	232
Db	415 TLNFLSSLTAHR----VTVT---QHVLA-----LTAPQGSNT NLLPKLF-----	452
Qy	233 AMTRELLRAQVPSSLGSLFNKKEN--KEVILKLLVIFENINDNF KWEENE-----PTQHQ	285
Db	453 -----ARILSALGSMKKANLYDDPTLATIFLLNNYNYIA KT LADEQDGLLPAITE	504
Qy	286 FGEGLFFFLKEFQVCADKXL---GIESHHDFLVKVVGKF MAK	326
Db	505 MNSNILSFYHEEIATCTNEYLKSWNGIASILKS VDRIGEDKQMAK	549

RESULT 7

A36682

72K mitochondrial outer membrane protein - Neurospora crassa

C;Species: Neurospora crassa

C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-Jul-2004

C;Accession: A36682

R;Steger, H.F.; Soellner, T.; Kiebler, M.; Dietmeier, K.A.; Pfaller, R.; Truelzsch, K.S.; Tropschug, M.; Neupert, W.; Pfanner, N.

J. Cell Biol. 111, 2353-2363, 1990

A;Title: Import of ADP/ATP carrier into mitochondria: two receptors act in parallel.

A;Reference number: A36682; MUID:91115930; PMID:2177474

A;Accession: A36682

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-619 <STE>

A;Cross-references: UNIPROT:P23231; GB:X53735; NID:g3027; PIDN:CAA37767.1; PID:g3028

C;Superfamily: mitochondrial outer membrane protein, 70K; tetratricopeptide repeat homology

C;Keywords: membrane protein; mitochondrion

F;131-163/Domain: tetratricopeptide repeat homology #status atypical <TT1>

F;164-197/Domain: tetratricopeptide repeat homology <TT2>

F;198-231/Domain: tetratricopeptide repeat homology <TT3>

F;335-368/Domain: tetratricopeptide repeat homology <TT4>

F;369-402/Domain: tetratricopeptide repeat homology <TT5>

F;403-436/Domain: tetratricopeptide repeat homology <TT6>

F;512-545/Domain: tetratricopeptide repeat homology <TT7>

F;546-579/Domain: tetratricopeptide repeat homology <TT8>

Query Match 6.4%; Score 109; DB 2; Length 619;  
Best Local Similarity 25.2%; Pred. No. 2.9;  
Matches 86; Conservative 40; Mismatches 129; Indels 86; Gaps 18;

Qy 31 IVWYPPWARIGTEAG---TRARARARARATRARRAVQKRASPNSDD--TVLSPQEL---- 81  
Db :||: ||:: ||| :|| :|| :|| :|| | | ||

Qy 56 VVYYLRKGSEQKESGPKLSKKERRKRKQAEKASTSKTEEAAPTQPKAASAVESADELPEID 115

Qy 82 -QKVLCLVEMSEKPYILEAALIALGNNA--AYAFNRDIIRDLGGLPIVAKILNTRDPIVK 138  
Db :|:|| ||| ||| ||| :||:|| ||| :|| | ||| :|| | ||| :|| | ||| :||

Qy 116 EESVVRLSEDERKAY--AAKLKEGNKAYGSKDFNKAI--DLYSKAIICK---PDPVYY 167

Qy 139 EKALIVLNNS---VNAENQRRLKVYMNVQCDDTITSRLNSSVQLAGLRLLTNMTVTNE 194  
Db ||:|| | |:||| :||:|| | :||| :||| :||| :||| :||| :||| :||| :||| :

Qy 168 SNRAACHNALAQWEQVADTTAALKLDPHYV--KALNRRANAYDQL-----SR 213

Qy 195 YQHML---ANSISdffrlfsagneetklqlvklllnlaenpamtrellraqvpslglsl 250  
Db ||:|| | |:||| ||| :||:|| | ||| :||:|| | :|| | |

Qy 214 YRHALLDFTASCIIDGFR----NEQSAQAVERLLKKFAENKA--KEILETKPPKLPSS 266

Qy 251 FNKKENKEVILKLLVIF-----ENINDNFKWEENEPTQNQFGEGLFFFKE----- 297  
Db | :|| | | :|| | | :||:|| | :|| | | :|| | |

Qy 267 F-----VGNYLQSFRSKPRPEGLEDSVELSE-----ETGLGQLQLGLKHLESKTGT 312

Qy 298 -----FQVCADKXLGIESHHDFLVKVKVGKFMAKLAEH 330

Db ||:|| | || | :|| | | | :|| |

Qy 313 GYEEGSAAFKKALD--LGELGPHEALAYNLGTFHCLMGKH 351

RESULT 8

B96625

hypothetical protein T2K10.12 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: B96625

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: B96625

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-867 <STO>

A;Cross-references: UNIPROT:Q9ZUI6; GB:AE005173; NID:g4249386; PIDN:AAD14483.1; GSPDB:GN00141

C;Genetics:

A;Gene: T2K10.12

A;Map position: 1

Query Match 6.3%; Score 108.5; DB 2; Length 867;  
Best Local Similarity 22.5%; Pred. No. 4.8;  
Matches 73; Conservative 39; Mismatches 96; Indels 117; Gaps 15;

Qy 41 GTEAGTRARA-RARARATRARRAVQK----RASPNSDD----- 73  
|| || || | | :| || | :|

Db 7 GTRLSDMIRAIRASKTAAEERAVVRKECAAIRASINENDQDYRHDLAKLMFIHMLGYPT 66

Qy 74 -----TVLSP-----QELQKVLCVEMSEK-----PYILEAAL 101  
: || .... | |:|| || | | ||: ||

Db 67 HFGQMECLKLIASPGFPEKRIGYLGIMLLDERQEVLMLVTNSLKQDLNHTNQYIVGLAL 126

Qy 102 IALGNNAAYAFNRDIIRDGLGPLIVAKILNTRDPIVKEKALI---VLNNLSVNAENQRR 157  
|||| : ||: | | ::| || ::|| : :: : :||

Db 127 CALGNICSAEMARDL-----APEVERLLQFRDPNIRKKAALCAIRIIRKVPDLSEN-- 177

Qy 158 LKVYMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTN---EYQHM-----LAN 201  
::| : : | : | : | : : || :||

Db 178 ---FINP--GAALLKEKHHGVЛИTGVHLCTEICKVSSEALEYFRKKCTEGLVKTLRDIAN 232

Qy 202 S-----ISDFFRFLFSAGNEETKLQVLKLLNLAEKPAMTRELLR---AQVPSSLG 248

Db	233 SPYSPEYDVAGITDPF-----LHIRLLKLLRVLGQGDADASDCMNDILAQVASKTE 283
Qy	249 SLFNKKENKEVILKLLVIFENINDN 273
Db	284 S--NKNAGNAILYECVQTIMSIEEN 306

## RESULT 9

T51951

gamma-adaptin 1 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C;Accession: T51951  
R;Schledzewski, K.; LaBrie, S.T.; Crawford, N.M.; Brinkmann, H.; Medel, R.R.  
submitted to the EMBL Data Library, April 1998  
A;Description: Sequencing of the Arabidopsis thaliana EST clone 203C19T7  
(Accession H77083) that is homologous to gamma-adaptin from mouse and *Ustilago*  
*maydis*.  
A;Reference number: Z25886  
A;Accession: T51951  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-876 <SCH>  
A;Cross-references: UNIPROT:O81227; EMBL:AF061286; PIDN:AAC28338.1  
A;Experimental source: cultivar Columbia

Query Match 6.3%; Score 107.5; DB 2; Length 876;  
Best Local Similarity 22.7%; Pred. No. 5.8;  
Matches 73; Conservative 35; Mismatches 99; Indels 115; Gaps 14;

Qy 44 AGTRARARARA-----RATRARRAVQK-----RASPNSDD----- 73  
:||||| | ||| | | | | :||| | ||| | |||

Qy 101 LIALGNNAAYAFNRDIIRDLGGPLIVAKILNTRDPIVKEKALIVLNNL-----SV 150  
| | || : ||: | | ::: || ::::|| : : : |  
Pb 126 LCALGNICSAEMARDI-----APFVERLTOFEDPNTRKKAAICSTTRKVKVDIAENEV 179

Qy 151 NA-----ENQRRLKVMNQVCDDTITSRLNSSV-----QLAGLRLLTNMTVTN 193  
           ||      |      :      :      |:      :      |      :      :      :  
 Ph 194 NAAASLKEKINHSLITCIVOLGKELST-----INDEM  EKEPTKCTESI  KLTIPRITNGMVR 237

Qy 194 EYQHMLANSISDFFRLFSAGNEETKLQLVKLLLNLAEVPAMTRELLR---AQVPSSLGSL 250  
|| |::| | :|| | : | :|: ||| : |

Qy 251 FNKKENKEVILKLLVIFENIND 272  
|| | : : : | |

B64075  
transcription initiation factor sigma 70 - Haemophilus influenzae (strain Rd KW20)  
C;Species: Haemophilus influenzae  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: B64075  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.  
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A;Accession: B64075  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-629 <TIGR>  
A;Cross-references: UNIPROT:P43766; GB:U32735; GB:L42023; NID:g1573509; PIDN: AAC22190.1; PID:g1573517; TIGR:HI0533  
C;Superfamily: transcription initiation factor sigma 70; transcription initiation factor sigma katF homology; transcription initiation factor sigma region 1 homology  
C;Keywords: DNA binding; sigma factor; transcription initiation  
F;1-143/Domain: transcription initiation factor sigma region 1 homology <SR1>  
F;397-623/Domain: transcription initiation factor sigma katF homology <KTF>

Query Match 6.2%; Score 107; DB 2; Length 629;  
Best Local Similarity 21.2%; Pred. No. 4.1;  
Matches 55; Conservative 37; Mismatches 94; Indels 74; Gaps 10;

Qy 3 DVDDAGDCSGARYNDWSDDDD-----DSNESKSIVWYPPWARIGTEAGRARARAR 55  
| || : || | |::| ||::| : | | : | :  
Db 192 DEDDEEESSNADVEDNEDEEDNESESTSDDSDSDN-----SIDPEVAREKFQQQLREQ 243

Qy 56 ATRARRAVQK--RASPNSDDTVLSPQELQK-----VLCLVEMSEKPYILEAAL 101  
:: :|| |: :| :| :| :|| :|| :: | |  
Db 244 HSKTLAVIEKHGRSGKRAQDQIALLGEIFKQFRLVPKQFDLLVLSMKEMMKRVRYQERQL 303

Qy 102 IALGNNAAYAFNRDIIRDGLGP-----IVAKILNTRDPIVK----E 139  
: |: |: |: |: | | : | | .. :  
Db 304 -----QKILVDIAGMPKDDFEKIITTNGSNEWVAKALKSSKPWAKRLIKYED 351

Qy 140 KALIVLNNLSVNAENQRRLKVYMNQVCD----DTITSRLNSSVQLAGLRLLTNMTVTNE 194  
: ||||:|: || : | :|| : | : | |||: :: :  
Db 352 RIYEALNNLAITEENTKLTTQMRDICDAVARGEQKARRAKKEMVEANLRLV--ISIAKK 409

Qy 195 YQHMLANSISDFFRLFSAGN 214  
| | | | | ||  
Db 410 Y----TNRGLQFLDLIQEGN 425

RESULT 11

F84471

hypothetical protein At2g05810 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: F84471

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: F84471

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-580 <STOP>

A;Cross-references: UNIPROT:Q8S8G1; GB:AE002093; NID:g6598505; PIDN:AAF18619.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g05810

A;Map position: 2

Query Match 6.2%; Score 106.5; DB 2; Length 580;  
Best Local Similarity 18.6%; Pred. No. 4;  
Matches 56; Conservative 52; Mismatches 86; Indels 107; Gaps 8;

Qy 67 ASPNSDDTVLSPQELQKVLCLEMSEKPYILEAALI----- 102  
Db :| :| || | :| :| :| :||:

Qy 103 -----ALGNNAAYAFNRDIIRDLGLGLPIVAKILNT----- 132  
Db |: | || | | : : | :|:: ::| :

Qy 133 -----RDPIVKKEKA---LIVLNNSLVNAENQRRLKVYMNQV-CDDTITSRLNSS- 177  
Db || ||::|: | | | | : : :|: :|::|: |::|: |::|

Qy 352 LISSSGEYYRDLIVRERGLQILIHVLQESSNPDTIEHCLLALSQISAMETVSRLVLSST 411

Qy 178 -----VQLAGLRLLTNMVTNEQHMLANSISDFRLFS---AGNEET 217  
Db :| | ||:|:|::: : :|:| || | | :|

Qy 412 RFIIRLGELIKHGNVILQQISTSLSNLTISDGNKRAVADCLSSLIRLMESPCKPAGLQEA 471

Qy 218 KLQVLKLLNLAEAPMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWE 277

Db : | || : | :|:| :| :| :| :| :| :| :| :| :| :|

Qy 472 ATEAAKSLLTVRSN---RKELMR-----DEKSVIRLVQMLDPRNERMNNK 513

Qy 278 E 278

|

Db 514 E 514

RESULT 12

A86416

probable arm repeat-containing protein - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: A86416

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Millscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A86416

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-729 <STO>

A;Cross-references: UNIPROT:Q9C7R6; GB:AE005172; NID:g10092208; PIDN:AAG12624.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

Query Match 6.2%; Score 106.5; DB 2; Length 729;  
Best Local Similarity 23.0%; Pred. No. 5.4;  
Matches 51; Conservative 39; Mismatches 101; Indels 31; Gaps 7;

Qy 68 SPNSDDTVLSPQELQVLCLVEMSEKPYILEAALIALGNNAAYAF-----N 113  
| || | : || :: : | : | : || | |

Db 386 SPNESFASALPTK----AAVEANKATVSILIKYLADGSQAAQTVAAREIRLLAKTGKEN 440

Qy 114 RDIIRDGLGLPIVAKILNTRDPIVKEKALIVLNNSVNAENQRRLKVYMNQVCDDTITSR 173  
| | : | : | : : | : | : | : | : | : | : | : | : | : | : | : |

Db 441 RAYIAEAGAIPLCRLLTSENAIAQENSVTAMLNLSIYEKNKSR--IMEEGDCLESIVSV 498

Qy 174 LNSSV---QLAGLRLLTNMTVTNEYQHMLA--NSISDFRFLSAGNEETKLQVLKLLL 226  
| | : | | : | : : | : | : | : | : | : | : |

Db 499 LVSGLTVEAQENAAATLFSLSAVHEYKKRIAIVDQCVEALALLLQNQTPRGKKDAVTALY 558

Qy 227 NLAENPAMTRELLRAQPSSL-GSLFNKKENKEV--ILKLLV 265

| | : | : | : | : | : | : | : | : |

Db 559 NLSTHPDNCSRMIEGGGVSSLVGALKNEGVAEEAAGALALLV 600

RESULT 13

T27763

hypothetical protein ZK177.5 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T27763  
R;Anderson, K.  
submitted to the EMBL Data Library, July 1995  
A;Description: The sequence of *C. elegans* cosmid ZK177.  
A;Reference number: Z20416  
A;Accession: T27763  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-428 <AND>  
A;Cross-references: EMBL:U21321; PIDN:AAB36969.1; GSPDB:GN00020; CESP:ZK177.5  
A;Experimental source: strain Bristol N2; clone ZK177  
C;Genetics:  
A;Gene: CESP:ZK177.5  
A;Map position: 2  
A;Introns: 55/1; 95/1; 133/2; 157/2; 232/2; 253/3; 338/2

Query Match 6.1%; Score 105; DB 2; Length 428;  
Best Local Similarity 23.5%; Pred. No. 3.5;  
Matches 57; Conservative 35; Mismatches 81; Indels 70; Gaps 10;

Qy	71 SDDTVLSPQELQKVLCVEM-----SEKPYILEAAALIALGNNAAYA----FNRD 115
	:    :     :    :  :  :    : :    :
Db	166 SNDLVCHVADQQKRGFLVDMQKVAGRWSLESAGQILFEKSLGSLGNRSEWADGLIELNK 225
Qy	116 II-----RDL--GGLPIVAKILNTRDPIVKEKALIVLN--NLSVNAENQRLKVYMNQVC 166
	:  :               ::    : :         ::
Db	226 IFQLSANKDMRFASYLINRKELNRRD--VKTAPMLIYNLYNLATHPE---ALKEIQKEIK 280
Qy	167 DDTITSRLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLL 226
	:  :  :    :    :  :  :  :  :  :  :  :
Db	281 EDPASSKLT-----FLRACIKETFRMFPIGTEVSRTQKNLIL 318
Qy	227 NLAENPAMTRELLRAQPVSSLGSLFNKKENKEVILKLLVIFENINDNFK---WEENEPTQ 283
	:          :    :    :    :
Db	319 SGYEVVPAGTAVDI-----NTNVLMRHEVLFSDSPREFKPQRWLEKSKEV 362
Qy	284 NQF 286
	:
Db	363 HPF 365

#### RESULT 14

S50541

hypothetical protein YER038c - yeast (*Saccharomyces cerevisiae*)

C;Species: *Saccharomyces cerevisiae*

C;Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S50541

R;Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A;Description: The sequence of *S. cerevisiae* cosmids 9379, 9581, and lambda clone 4678.

A;Reference number: S50432

A;Accession: S50541

A;Molecule type: DNA

A;Residues: 1-464 <DIE>

A;Cross-references: UNIPROT:P40026; EMBL:U18796; NID:g603265; PID:g603271;  
GSPDB:GN00005; MIPS:YER038c

C;Genetics:

A;Gene: SGD:KRE29; MIPS:YER038c

A;Cross-references: SGD:S0000840

A;Map position: 5R

C;Superfamily: *Saccharomyces cerevisiae* hypothetical protein YER038c

Query Match 6.1%; Score 104; DB 2; Length 464;  
Best Local Similarity 18.8%; Pred. No. 4.6;  
Matches 68; Conservative 57; Mismatches 110; Indels 126; Gaps 15;

Qy 20 DDDDSNESKSIVWYPPWARIGTE-----AGTRARARARARATRARRAVQKR 66  
Db 38 DDDDEKVHPNFISDPENDSLSDEEFSSLNSDNLNGAKAESGDDFDPILKRTIISKR 97

Qy 67 ASPNS---DDTVLSPQELQKVLCVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGL 123  
Db 98 KAPSNNEDEEIVKTPRKLNVYVPL-----KIFNLGD----SFDDTI----T 135

Qy 124 PIVAKILNTRDPIV---KEKALIVLNNLSVNAENQRRLK-----VYMNQVCDDTITS 172  
Db 136 TTVAKLQDLKKEILDSPRSNKSIVITSNTVAKSELQKSIKFSGSIPEIYLDVVTKETISD 195

Qy 173 RLNS-----SVQLAGLRL-----LTNMTVTNEYQHMLANSISDFRFLFSA 212  
Db 196 KYKDWHFISKNCHYEQLMDLEMKDTAYSFLFGSSRSQGKVPEFVHLKCPSTNLLVFGV 255

Qy 213 GNEETKLQLKLLLNLNAENPAMTRELLRAQPSSLGSLFNKKENKEV-----IL 261  
Db 256 NQEKC-----NSLKINYEKKENSRYDNLCTIFPVNKML 288

Qy 262 KLLVIFENINDNFKWEEENEPTQNQFGEGLFFLKEFQVC--ADKXL--GIESHHDFLVK 317  
Db 289 KFLMYFYSDDDNDDVRE-----FFLKAF-ICLILDRKVFNAMESDHRLCFK 333

Qy 318 V 318  
Db 334 V 334

RESULT 15

E82909

conserved hypothetical UU292 [imported] - *Ureaplasma urealyticum*

C;Species: *Ureaplasma urealyticum*

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C;Accession: E82909

R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to GenBank, February 2000

A;Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a minimal genome and sexually transmitted pathogen.

A;Reference number: A82870

A;Accession: E82909

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1830 <GLA>

A;Cross-references: GB:AE002127; GB:AF222894; NID:g6899268; PIDN:AAF30701.1;  
GSPDB:GN00123; UUSP:UU292

A;Experimental source: serovar 3; biovar 1

C;Genetics:

A;Gene: UU292

A;Genetic code: SGC3

Query Match 6.1%; Score 104; DB 2; Length 1830;  
Best Local Similarity 19.5%; Pred. No. 27;  
Matches 65; Conservative 52; Mismatches 96; Indels 120; Gaps 14;

Qy	77 SPQELQKVLCVEMSE---KPY--ILEAALIALGNNAAYAFNRDIIRDLGGLPIVAKILN 131 : :::  :  :::   :   :    :      : :	
Db	1400 TPEKVLKISSLLDINEIDARDYADIIEIIILVEIGFNVTSIQNNDVNNN-----LK 1449	
Qy	132 TRDPIVKEKALIVLN---NLSVNAENQRRLKVMNQVCDDTITSRLNSS---VQLAGLR- 184     :  :  :    :  :  :  :  :  :  :  :	
Db	1450 TIDKKTNDFAQILKKALNNGVSDQQLQKIKNVVNYYLDDIVKIHDSSSFLRIQLEQLSH 1509	
Qy	185 -----LLTNMTVTNEYQHMLA-----NS 202   :: : ::  :  :	
Db	1510 VLVDKITAVLPKSLTIKHKYTKIFSSILNNQDFLQKAKTLLSTILNELIDHKDKYKDINS 1569	
Qy	203 ISdffrlfsagn-EETKLQVLKLLLNLAEVPAMTRELLRAQVPSSLGSLFNKKENKEVIL 261  : :  :   :    :  :  :  :  :	
Db	1570 FSELISVFFKNKASDLKTQLKDLLNTILKNQTLITNIGQVIIESF-----KLENKISIL 1623	
Qy	262 -----KL-----LVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVCA 302  :    :  :	
Db	1624 DSDLEQNTISFINKIAHITELPIYTNLVDNF-----FNFFSEYTKSS 1666	
Qy	303 D-KXLGIESHHDFLVKVKVGKFMAKLAEHMFpk 334          :  :  :	
Db	1667 DTKTLNF-----NKFKSSLFQAIIPk 1687	

Search completed: January 7, 2005, 14:52:28

Job time : 21.1939 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 7, 2005, 14:51:07 ; Search time 63.3717 Seconds  
(without alignments)  
1917.457 Million cell updates/sec

Title: US-10-726-721A-9

Perfect score: 1715

Sequence: 1 RGDVDDAGDCSGARYNDWSD.....VKVGKFMAKILAEHMFPKSQE 337

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1713	99.9	337	9	US-09-780-996-9	Sequence 9, Appli
2	1713	99.9	337	16	US-10-726-721-9	Sequence 9, Appli
3	1708	99.6	342	16	US-10-408-765A-834	Sequence 834, App
4	1708	99.6	379	14	US-10-028-072-216	Sequence 216, App
5	1708	99.6	379	14	US-10-140-808-216	Sequence 216, App
6	1708	99.6	379	14	US-10-121-049-216	Sequence 216, App
7	1708	99.6	379	14	US-10-123-904-216	Sequence 216, App
8	1708	99.6	379	14	US-10-140-470-216	Sequence 216, App
9	1708	99.6	379	14	US-10-175-746-216	Sequence 216, App
10	1708	99.6	379	14	US-10-176-918-216	Sequence 216, App
11	1708	99.6	379	14	US-10-176-921-216	Sequence 216, App
12	1708	99.6	379	14	US-10-137-865-216	Sequence 216, App
13	1708	99.6	379	14	US-10-140-474-216	Sequence 216, App
14	1708	99.6	379	14	US-10-142-431-216	Sequence 216, App
15	1708	99.6	379	14	US-10-143-114-216	Sequence 216, App
16	1708	99.6	379	14	US-10-140-002-216	Sequence 216, App
17	1708	99.6	379	14	US-10-142-419-216	Sequence 216, App
18	1708	99.6	379	14	US-10-123-262-216	Sequence 216, App
19	1708	99.6	379	14	US-10-142-423-216	Sequence 216, App
20	1708	99.6	379	14	US-10-121-050-216	Sequence 216, App
21	1708	99.6	379	14	US-10-141-755-216	Sequence 216, App
22	1708	99.6	379	14	US-10-143-032-216	Sequence 216, App
23	1708	99.6	379	14	US-10-123-108-216	Sequence 216, App
24	1708	99.6	379	14	US-10-123-236-216	Sequence 216, App
25	1708	99.6	379	14	US-10-123-261-216	Sequence 216, App
26	1708	99.6	379	14	US-10-140-921-216	Sequence 216, App
27	1708	99.6	379	14	US-10-140-928-216	Sequence 216, App
28	1708	99.6	379	14	US-10-121-045-216	Sequence 216, App
29	1708	99.6	379	14	US-10-123-292-216	Sequence 216, App
30	1708	99.6	379	14	US-10-123-903-216	Sequence 216, App
31	1708	99.6	379	14	US-10-124-819-216	Sequence 216, App
32	1708	99.6	379	14	US-10-124-822-216	Sequence 216, App
33	1708	99.6	379	14	US-10-140-925-216	Sequence 216, App
34	1708	99.6	379	14	US-10-160-498-216	Sequence 216, App
35	1708	99.6	379	14	US-10-124-824-216	Sequence 216, App
36	1708	99.6	379	14	US-10-127-825A-216	Sequence 216, App
37	1708	99.6	379	14	US-10-127-829A-216	Sequence 216, App
38	1708	99.6	379	14	US-10-127-835A-216	Sequence 216, App
39	1708	99.6	379	14	US-10-127-839A-216	Sequence 216, App
40	1708	99.6	379	14	US-10-127-901A-216	Sequence 216, App
41	1708	99.6	379	14	US-10-128-693A-216	Sequence 216, App
42	1708	99.6	379	14	US-10-131-813A-216	Sequence 216, App
43	1708...	99.6	379	14	US-10-131-818A-216	Sequence 216, App
44	1708	99.6	379	14	US-10-131-823A-216	Sequence 216, App
45	1708	99.6	379	14	US-10-131-824A-216	Sequence 216, App

#### ALIGNMENTS

RESULT 1  
 US-09-780-996-9  
 ; Sequence 9, Application US/09780996  
 ; Patent No. US20020061553A1

; GENERAL INFORMATION:  
; APPLICANT: Maury, Isabella  
; APPLICANT: Mercken, Luc  
; APPLICANT: Fournier, Alain  
; TITLE OF INVENTION: Partners of the PTB1 Domain of FE65, Preparation and Uses  
; FILE REFERENCE: ST00004-US  
; CURRENT APPLICATION NUMBER: US/09/780,996  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: FR00/01628  
; PRIOR FILING DATE: 2000-02-10  
; PRIOR APPLICATION NUMBER: US 60/198,500  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: X=G, D, V, or A  
US-09-780-996-9

Query Match 99.9%; Score 1713; DB 9; Length 337;  
Best Local Similarity 100.0%; Pred. No. 4.6e-157;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRAR 60  
Db 1 RGDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRAR 60

Qy 61 RAVQKRASPNSDDTVLSPQELQVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDL 120  
Db 61 RAVQKRASPNSDDTVLSPQELQVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDL 120

Qy 121 GGLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQL 180  
Db 121 GGLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQL 180

Qy 181 AGLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLNLAEVPAMTRELLR 240  
Db 181 AGLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLNLAEVPAMTRELLR 240

Qy 241 AQVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQV 300  
Db 241 AQVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQV 300

Qy 301 CADKXLGIESHHDFLVVKVGKFMAKLAEHMFPKSQE 337  
Db 301 CADKXLGIESHHDFLVVKVGKFMAKLAEHMFPKSQE 337

RESULT 2  
US-10-726-721-9  
; Sequence 9, Application US/10726721  
; Publication No. US20040166109A1  
; GENERAL INFORMATION:

; APPLICANT: Maury, Isabella  
; APPLICANT: Mercken, Luc  
; APPLICANT: Fournier, Alain  
; TITLE OF INVENTION: Partners of the PTB1 Domain of FE65, Preparation and Uses  
; FILE REFERENCE: ST00004-US  
; CURRENT APPLICATION NUMBER: US/10/726,721  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: US/09/780,996A  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: FR00/01628  
; PRIOR FILING DATE: 2000-02-10  
; PRIOR APPLICATION NUMBER: US 60/198,500  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: X=G, D, V, or A  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (305)..(305)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-10-726-721-9

Query Match 99.9%; Score 1713; DB 16; Length 337;  
Best Local Similarity 100.0%; Pred. No. 4.6e-157;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RGDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRAR 60
Db	1 RGDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRAR 60
Qy	61 RAVQKRASPNSDDTVLSPQELQVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDL 120
Db	61 RAVQKRASPNSDDTVLSPQELQVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDL 120
Qy	121 GGLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRLKVYMNQVCDDTITSRLNSSVQL 180
Db	121 GGLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRLKVYMNQVCDDTITSRLNSSVQL 180
Qy	181 AGLRLLTNMVTNEYQHMLANSISDFRFLSAGNEETKLQLVKLLLNLAEHPAMTRELLR 240
Db	181 AGLRLLTNMVTNEYQHMLANSISDFRFLSAGNEETKLQLVKLLLNLAEHPAMTRELLR 240
Qy	241 AQVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQV 300
Db	241 AQVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQV 300
Qy	301 CADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 337
Db	301 CADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 337

RESULT 3  
US-10-408-765A-834  
; Sequence 834, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 834  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-834

Query Match 99.6%; Score 1708; DB 16; Length 342;  
Best Local Similarity 99.7%; Pred. No. 1.4e-156;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
Db 7 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 66

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 67 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 126

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
Db 127 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 186

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
Db 187 GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA 246

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 301  
Db 247 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 306

Qy 302 ADKXLGIESHHDFLVKVVGKFMAKLAEHMFPKSQE 337  
Db 307 ADKVLGIESHHDFLVKVVGKFMAKLAEHMFPKSQE 342

RESULT 4  
US-10-028-072-216  
; Sequence 216, Application US/10028072

; Publication No. US20030004311A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang  
; TITLE OF INVENTION:  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/028,072  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059836  
; PRIOR FILING DATE: 1997-09-24  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062285  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062814  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/062816  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063045  
; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063082  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/063127  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063327  
; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: 60/063329  
; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: 60/063550  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063561  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063704  
; PRIOR FILING DATE: 1997-10-29  
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; PRIOR APPLICATION NUMBER: 60/063738  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063755  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064248  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/064809  
; PRIOR FILING DATE: 1997-11-07  
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; PRIOR APPLICATION NUMBER: 60/066453  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066511  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/069212  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069278  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069334  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069694  
; PRIOR FILING DATE: 1997-12-16  
; PRIOR APPLICATION NUMBER: 60/072320  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: 60/073612  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR APPLICATION NUMBER: 60/074086  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/074092  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-02-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081695  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081818  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082999  
; PRIOR FILING DATE: 1998-04-24  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085149  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/086414  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/086430  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/088026  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088730  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088741  
; PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 19/98-06-11  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090538  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07

Query Match 99.68; Score 1708; DB 14; Length 379;  
Best Local Similarity 99.78; Pred. No. 1.7e-156;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
|||.....|||.....|||.....|||.....|||.....|||.....|||.....|||.....|||.....|||  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELOQVLCLEVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
|||||

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNVQCDDTITSRLNSSVQLA 181

Qy . . . 182 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQLVLKLLLNLAENPAMTRELLRA 241

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301

Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337

Db 344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379



Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKEEENEPTQNQFGEGLFFLKEFQVC 343  
|||  
Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
|||  
Db 344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

RESULT 6  
US-10-121-049-216  
; Sequence 216, Application US/10121049  
; Publication No. US20030022239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C17  
; CURRENT APPLICATION NUMBER: US/10/121,049  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 216  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-121-049-216

Query Match 99.6%; Score 1708; DB 14; Length 379;  
Best Local Similarity 99.7%; Pred. No. 1.7e-156;  
Matches 335; Conservative 0; Mismatches 1;..Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
|||  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103  
|||  
Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
|||  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163  
|||  
Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
|||

Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223  
Qy 182 GLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLOVLKLLLNLAEVPAMTRELLRA 241  
| |||||||  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLOVLKLLLNLAEVPAMTRELLRA 283  
Qy 242 QVPSSLGSLFNKKENKEVILKLIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
| |||||||  
Db 284 QVPSSLGSLFNKKENKEVILKLIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343  
Qy 302 ADKXLGIESHHDFLVKVKGKFMKLAEHMFPKSQE 337  
| |||  
Db 344 ADKVLGIESHHDFLVKVKGKFMKLAEHMFPKSQE 379

RESULT 7

US-10-123-904-216

; Sequence 216, Application US/10123904

; Publication No. US20030022328A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C54

; CURRENT APPLICATION NUMBER: US/10/123,904

; CURRENT FILING DATE: 2002-04-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 216

; LENGTH: 379

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-123-904-216

Query Match 99.6%; Score 1708; DB 14; Length 379;  
Best Local Similarity 99.7%; Pred. No. 1.7e-156;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
| |||||||

Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 103

Qy	62	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
Db	104	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
Qy	122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	181
Db	164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	223
Qy	182	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA	241
Db	224	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA	283
Qy	242	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	301
Db	284	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	343
Qy	302	ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE	337
Db	344	ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE	379

RESULT 8

US-10-140-470-216

; Sequence 216, Application US/10140470

; Publication No. US20030022331A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C160

; CURRENT APPLICATION NUMBER: US/10/140,470

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 216

; LENGTH: 379

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-140-470-216

Query Match 99.6%; Score 1708; DB 14; Length 379;  
 Best Local Similarity 99.7%; Pred. No. 1.7e-156;  
 Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	2	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR	61
Db	44	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR	103
Qy	62	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
Db	104	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
Qy	122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	181
Db	164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	223
Qy	182	GLRLLTNMTVTNEYQHMLANSISDFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA	241
Db	224	GLRLLTNMTVTNEYQHMLANSISDFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA	283
Qy	242	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	301
Db	284	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	343
Qy	302	ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE	337
Db	344	ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE	379

#### RESULT 9

US-10-175-746-216

; Sequence 216, Application US/10175746

; Publication No. US20030027270A1

#### ; GENERAL INFORMATION:

;
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin

;
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ;
 TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ;
 FILE REFERENCE: P3330R1C353  
 ;
 CURRENT APPLICATION NUMBER: US/10/175,746  
 ;
 CURRENT FILING DATE: 2002-06-19  
 ;
 Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 216  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-175-746-216

Query Match 99.6%; Score 1708; DB 14; Length 379;  
Best Local Similarity 99.7%; Pred. No. 1.7e-156;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQVKLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 104 AVQKRASPNSDDTVLSPQELQVKLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA 283

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343

Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

#### RESULT 10

US-10-176-918-216

; Sequence 216, Application US/10176918  
; Publication No. US20030027275A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C382  
; CURRENT APPLICATION NUMBER: US/10/176,918  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 216  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-918-216

```

Query Match          99.6%;  Score 1708;  DB 14;  Length 379;
Best Local Similarity  99.7%;  Pred. No. 1.7e-156;
Matches 335;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 61
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 103

Qy      62 AVQKRASPNSDDTVLSPQELQVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      104 AVQKRASPNSDDTVLSPQELQVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163

Qy      122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNVQVCDDTITSRLNSSVQLA 181
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNVQVCDDTITSRLNSSVQLA 223

Qy      182 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLNLAEAPAMTRELLRA 241
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      224 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLNLAEAPAMTRELLRA 283

Qy      242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301
       ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343

Qy      302 ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 337
       ||| | | | | | | | | | | | | | | | | | | |
Db      344 ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE 379

```

## RESULT 11

; Sequence 216, Application US/10176921  
; Publication No. US20030027276A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney,Austin L.  
; APPLICANT: Sherwood,Steven  
; APPLICANT: Smith,Victoria  
; APPLICANT: Stewart,Timothy A.  
; APPLICANT: Tumas,Daniel  
; APPLICANT: Watanabe,Colin K  
; APPLICANT: Wood,William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C288  
; CURRENT APPLICATION NUMBER: US/10/176,921  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 216  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-921-216

Query Match 99.6%; Score 1708; DB 14; Length 379;  
Best Local Similarity 99.7%; Pred. No. 1.7e-156;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	61
Db	44	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	103
QY	62	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
Db	104	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
QY	122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA	181
Db	164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA	223
QY	182	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA	241
Db	224	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNAENPAMTRELLRA	283
QY	242	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	301
Db	284	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	343
QY	302	ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE	337
Db	344	ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE	379

RESULT 12

US-10-137-865-216  
; Sequence 216, Application US/10137865  
; Publication No. US20030032155A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C154  
; CURRENT APPLICATION NUMBER: US/10/137,865  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 216  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-137-865-216

Query Match 99.6%; Score 1708; DB 14; Length 379;  
Best Local Similarity 99.7%; Pred. No. 1.7e-156;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 61  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163

Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFRFLSAGNEETKLQVLKLLNLAEFPAMTRELLRA 241  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFRFLSAGNEETKLQVLKLLNLAEFPAMTRELLRA 283

Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 301  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 343

Qy 302 ADKXLGIESHHDFLVVKVGKFMAKLAEHMFPKSQE 337  
Db 344 ADKVLGIESHHDFLVVKVGKFMAKLAEHMFPKSQE 379

RESULT 13  
US-10-140-474-216  
; Sequence 216, Application US/10140474  
; Publication No. US20030032156A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C162  
; CURRENT APPLICATION NUMBER: US/10/140,474  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 216  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien

Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 343  
Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
||| |||||||||||||||||||||||||||||||||  
Db 344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

RESULT 14

US-10-142-431-216

; Sequence 216, Application US/10142431

; Publication No. US20030036179A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C251  
; CURRENT APPLICATION NUMBER: US/10/142,431  
; CURRENT FILING DATE: 2002-05-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 216  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-142-431-216

Query Match 99.6%; Score 1708; DB 14; Length 379;  
Best Local Similarity 99.7%; Pred. No. 1.7e-156;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
||| |||||||||||||||||||||||||||||||||  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103  
Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
||| |||||||||||||||||||||||||||||||||  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163  
Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 181  
||| |||||||||||||||||||||||||||||  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 223

Qy 182 GLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQLKLLNLAEVPAMTRELLRA 241  
|||  
Db 224 GLRLLTNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQLKLLNLAEVPAMTRELLRA 283  
  
Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
|||  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343  
  
Qy 302 ADKXLGIESHHDFLVKVKGKFMALKLAEHMFPKSQE 337  
|||  
Db 344 ADKVLGIESHHDFLVKVKGKFMALKLAEHMFPKSQE 379

RESULT 15

US-10-143-114-216

; Sequence 216, Application US/10143114

; Publication No. US20030036180A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C211

; CURRENT APPLICATION NUMBER: US/10/143,114

; CURRENT FILING DATE: 2002-05-09

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 216

; LENGTH: 379

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-143-114-216

Query Match 99.6%; Score 1708; DB 14; Length 379;  
Best Local Similarity 99.7%; Pred. No. 1.7e-156;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
|||  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
|||  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163  
  
Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 181  
|||  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA 223  
  
Qy 182 GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrellra 241  
|||  
Db 224 GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrellra 283  
  
Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 301  
|||  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC 343  
  
Qy 302 ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 337  
|||  
Db 344 ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE 379

Search completed: January 7, 2005, 15:01:14

Job time : 64.3717 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2005, 12:37:55 ; Search time 69.2668 Seconds  
(without alignments)  
2799.340 Million cell updates/sec

Title: US-10-726-721A-9

Perfect score: 1715

Sequence: 1 RGDVDDAGDCSGARYNDWSD.....VKVGKFMALKLAEHMFPKSQE 337

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:  
1: uniprot\_sprot:  
2: uniprot\_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	1708	99.6	342	2	Q7L8L7 Q71817 homo sapien
2	1708	99.6	379	2	Q9UH62 Q9uh62 homo sapien
3	1708	99.6	379	2	AAQ89438 AAq89438 homo sapi
4	1645	95.9	379	2	Q8BHS6 Q8bhs6 mus musculu
5	1645	95.9	379	2	Q91VP8 Q91vp8 mus musculu
6	1625	94.8	379	2	Q9DC32 Q9dc32 mus musculu
7	781.5	45.6	453	2	Q9P291 Q9p291 homo sapien
8	766.5	44.7	456	2	Q9CX83 Q9cx83 mus musculu
9	766.5	44.7	456	2	AAH68228 Aah68228 mus muscu
10	683	39.8	632	2	Q7L311 Q71311 homo sapien
11	683	39.8	710	2	O60267 O60267 homo sapien
12	683	39.8	710	2	BAA25438 Baa25438 homo sapi
13	671.5	39.2	308	2	Q9BTM6 Q9btm6 homo sapien
14	670.5	39.1	308	2	Q8IZC1 Q8izc1 homo sapien
15	664	38.7	784	2	Q8BJ82 Q8bj82 m mus muscu

16	663.5	38.7	343	2	Q8N2F6	Q8n2f6 homo sapien
17	663	38.7	324	2	Q91VZ8	Q91vz8 mus musculu
18	663	38.7	722	2	Q8BTE9	Q8bte9 m mus muscu
19	663	38.7	784	2	Q8BJ81	Q8bj81 mus musculu
20	663	38.7	784	2	Q8BTE8	Q8bte8 mus musculu
21	663	38.7	784	2	Q9CXI9	Q9cxi9 m mus muscu
22	641.5	37.4	306	2	Q9CZ87	Q9cz87 mus musculu
23	640.5	37.3	306	2	Q9D0L7	Q9d0l7 mus musculu
24	640.5	37.3	306	2	AAH58573	Aah58573 mus muscu
25	640.5	37.3	306	2	AAH38487	Aah38487 mus muscu
26	623.5	36.4	388	2	Q9CUN3	Q9cun3 mus musculu
27	575.5	33.6	995	2	Q8K2R3	Q8k2r3 mus musculu
28	573.5	33.4	340	2	Q8R103	Q8r103 mus musculu
29	545.5	31.8	212	2	Q75ML8	Q75ml8 homo sapien
30	545.5	31.8	212	2	AAS07531	Aas07531 homo sapi
31	543.5	31.7	367	2	Q9H2Q0	Q9h2q0 homo sapien
32	452	26.4	249	2	Q8IZC3	Q8izc3 homo sapien
33	445	25.9	284	2	Q8IZC2	Q8izc2 homo sapien
34	389	22.7	283	2	Q9BVZ3	Q9bvz3 homo sapien
35	389	22.7	558	2	Q6P1M9	Q6plm9 homo sapien
36	389	22.7	558	2	Q9H969	Q9h969 homo sapien
37	389	22.7	558	2	AAH58904	Aah58904 homo sapi
38	389	22.7	558	2	AAH64983	Aah64983 homo sapi
39	354.5	20.7	497	2	Q8R0B3	Q8r0b3 mus musculu
40	346.5	20.2	300	2	Q7L4S7	Q7l4s7 homo sapien
41	346.5	20.2	300	2	AAH07677	Aah07677 homo sapi
42	346.5	20.2	321	2	Q9NTS2	Q9nts2 homo sapien
43	345	20.1	1404	2	O43168	O43168 homo sapien
44	330.5	19.3	236	2	Q9NWJ3	Q9nwj3 homo sapien
45	328.5	19.2	301	2	Q6TEL9	Q6tel9 brachydanio

#### ALIGNMENTS

##### RESULT 1

Q7L8L7

ID Q7L8L7 PRELIMINARY; PRT; 342 AA.  
 AC Q7L8L7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE DJ545K15.2 (ALEX3 (Protein similar to KIAA0512 and KIAA0443)) (BM-017).  
 GN Name=dJ545K15.2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wilson S.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=20499367; PubMed=11042152;

RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,  
 RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,  
 RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;  
 RT "Cloning and functional analysis of cDNAs with open reading frames for  
 RT 300 previously undefined genes expressed in CD34+ hematopoietic  
 RT stem/progenitor cells.";  
 RL Genome Res. 10:1546-1560(2000).  
 DR EMBL; AL121883; CAB92763.1; -.  
 DR EMBL; AF208859; AAF64273.1; -.  
 DR InterPro; IPR008938; ARM.  
 DR InterPro; IPR000225; Armadillo.  
 DR InterPro; IPR006911; DUF634.  
 DR Pfam; PF04826; DUF634; 1.  
 DR PROSITE; PS50176; ARM\_REPEAT; 1.  
 SQ SEQUENCE 342 AA; 38399 MW; 6158B311FE7CB5FB CRC64;  
  
 Query Match 99.6%; Score 1708; DB 2; Length 342;  
 Best Local Similarity 99.7%; Pred. No. 3.9e-118;  
 Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0  
  
 Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
 |||||||  
 Db 7 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 66  
  
 Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
 |||||||  
 Db 67 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 126  
  
 Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
 |||||||  
 Db 127 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 186  
  
 Qy 182 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA 241  
 |||||||  
 Db 187 GLRLLTNMTVTNEYQHMLANSISDFFRFLSAGNEETKLQVLKLLLNAENPAMTRELLRA 246  
  
 Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 301  
 |||||||  
 Db 247 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 306  
  
 Qy 302 ADKXLGIESHHDFLVKVKGKFMALKLAEHMFPKSQE 337  
 |||||  
 Db 307 ADKVLGIESHHDFLVKVKGKFMALKLAEHMFPKSQE 342

## RESULT 2

Q9UH62

ID Q9UH62 PRELIMINARY; PRT; 379 AA.

AC Q9UH62; Q9NPE4;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation

DE Hypothetical protein (ALEX3 protein).

GN Name=ARMCX3; Synonyms=alex3; ORFNames=UNQ2517;

OS     *Homo sapiens* (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Nicolas G., Galand C., Lecomte M.-C.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=21092608; PubMed=11162520;  
RA Kurochkin I.V., Yonemitsu N., Funahashi S., Nomura H.;  
RT "ALEX1, a novel human armadillo repeat protein that is expressed

RT differentially in normal tissues and carcinomas.";  
 RL Biochem. Biophys. Res. Commun. 280:340-347(2001).  
 DR EMBL; AF211175; AAF24487.1; -.  
 DR EMBL; BC005194; AAH05194.1; -.  
 DR EMBL; AY359079; AAQ89438.1; -.  
 DR EMBL; AB039669; BAA94602.1; -.  
 DR InterPro; IPR008938; ARM.  
 DR InterPro; IPR000225; Armadillo.  
 DR InterPro; IPR006911; DUF634.  
 DR Pfam; PF04826; DUF634; 1.  
 DR PROSITE; PS50176; ARM\_REPEAT; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 379 AA; 42500 MW; B715D7F83DF4DFB0 CRC64;

Query Match 99.6%; Score 1708; DB 2; Length 379;  
 Best Local Similarity 99.7%; Pred. No. 4.5e-118;  
 Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	2	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	61
Db	44	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	103
Qy	62	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
Db	104	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
Qy	122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA	181
Db	164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA	223
Qy	182	GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrellra	241
Db	224	GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrellra	283
Qy	242	QPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	301
Db	284	QPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	343
Qy	302	ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE	337
Db	344	ADKVLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE	379

### RESULT 3

AAQ89438

ID AAQ89438 PRELIMINARY; PRT; 379 AA.  
 AC AAQ89438;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ALEX3.  
 GN UNQ2517.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
RX PubMed=12975309;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.;  
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A  
RT Bioinformatics Assessment.";  
RL Genome Res. 13:2265-2270 (2003).  
DR EMBL; AY359079; AAQ89438.1; -.  
SQ SEQUENCE 379 AA; 42500 MW; B715D7F83DF4DFB0 CRC64;

Query Match 99.6%; Score 1708; DB 2; Length 379;  
Best Local Similarity 99.7%; Pred. No. 4.5e-118;  
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61  
| |||||||  
Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103  
  
Qy 62 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 121  
| |||||||  
Db 104 AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG 163  
  
Qy 122 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 181  
| |||||||  
Db 164 GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA 223  
  
Qy 182 GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrellra 241  
| |||||||  
Db 224 GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrellra 283  
  
Qy 242 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 301  
| |||||||  
Db 284 QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC 343  
  
Qy 302 ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPSQE 337  
| |||  
Db 344 ADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPSQE 379

#### RESULT 4

##### Q8BHS6

ID Q8BHS6 PRELIMINARY; PRT; 379 AA.  
AC Q8BHS6;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched  
DE library, clone:5730422G06 product:HYPOTHETICAL 42.5 kDa PROTEIN  
DE (ALEX3) (ALEX3 PROTEIN) homolog (ALEX3 protein).

GN Name=1200004E24Rik; Synonyms=Armcx3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RC STRAIN=Mix FVB/N;

RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [8]

RP SEQUENCE FROM N.A.

RC STRAIN=Mix FVB/N;

RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RA Strausberg R.;

RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AK030729; BAC27102.1; -.

DR EMBL; BC051113; AAH51113.1; -.

DR MGD; MGI:1918953; 1200004E24Rik.

DR InterPro; IPR008938; ARM.

DR InterPro; IPR000225; Armadillo.

DR InterPro; IPR006911; DUF634.

DR Pfam; PF04826; DUF634; 1.

DR PROSITE; PS50176; ARM\_REPEAT; 1.

KW Hypothetical protein.

SQ SEQUENCE 379 AA; 42619 MW; 6EA7B87544652055 CRC64;

Query Match 95.9%; Score 1645; DB 2; Length 379;

Best Local Similarity 95.8%; Pred. No. 2e-113;

Matches 322; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 61

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 44 GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR 103

Qy	62	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
Db	104	AVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
Qy	122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLA	181
Db	164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVYMNQVCDDTTSRLNSSVQLA	223
Qy	182	GLRLLTNMTVTNEYQHMLANSISdffrlfsagneetklqlvklllnlaenpamtrellra	241
Db	224	GLRLLTNMTVTNEYQHILANSISdffrlfsagneetklqlvklllnlaenpamtrellra	283
Qy	242	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVC	301
Db	284	QVPSSLGSLFNKKEYKEVILKLLIIFENINDNFKWEENEPAQNHFSEGSLFFLKEFQVC	343
Qy	302	ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE	337
	:     :		
Db	344	ADKVLGIESRHDQVRVKVGKFVAKLTERMFPKSQE	379

#### RESULT 5

Q91VP8

ID Q91VP8 PRELIMINARY; PRT; 379 AA.  
 AC Q91VP8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE ALEX3 protein.  
 GN Name=Armcx3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Mix FVB/N;  
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC011101; AAH11101.1; -.  
DR MGD; MGI:1918953; 1200004E24Rik.  
DR InterPro; IPR008938; ARM.  
DR InterPro; IPR000225; Armadillo.  
DR InterPro; IPR006911; DUF634.  
DR Pfam; PF04826; DUF634; 1.  
DR PROSITE; PS50176; ARM\_REPEAT; 1.  
SQ SEQUENCE 379 AA; 42649 MW; CE1EC87045695156 CRC64;

Query Match 95.9%; Score 1645; DB 2; Length 379;  
Best Local Similarity 95.8%; Pred. No. 2e-113;  
Matches 322; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy	2	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	61
Db	44	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	103
Qy	62	AVQKRASPNSDDTVLSPQELQVKLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
Db	104	AVQKRASPNSDDTVLSPQELQVKLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
Qy	122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	181
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Db	164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTTSRLNSSVQLA	223
Qy	182	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLLNLAEQPAMTRELLRA	241
		:	
Db	224	GLRLLTNMTVTNEYQHILANSISDFTRLFSAGNEETKLQVLKLLLNLAEQPAMTRELLRA	283
		:	
Qy	242	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	301
		:	
Db	284	QVPSSLGSLFNKKEYKEVILKLLIIFENINDNFKWEENEPAQNHFSEGSLFFFKEFQVC	343
		:	
Qy	302	ADKXLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE	337
		:       :	
Db	344	ADKVLGIESRHDQVRVKVGKFVAKLTERMFPKSQE	379

## RESULT 6

Q9DC32

ID Q9DC32 PRELIMINARY; PRT; 379 AA.  
AC Q9DC32;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,  
DE clone:1200004E24 product:HYPOTHETICAL 42.5 kDa PROTEIN (ALEX3) (ALEX3  
DE PROTEIN) homolog.

GN Name=1200004E24Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AK004598; BAB23399.1; -.  
 DR MGD; MGI:1918953; 1200004E24Rik.  
 DR InterPro; IPR008938; ARM.  
 DR InterPro; IPR000225; Armadillo.  
 DR InterPro; IPR006911; DUF634.  
 DR Pfam; PF04826; DUF634; 1.  
 DR PROSITE; PS50176; ARM\_REPEAT; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 379 AA; 42662 MW; F40A039CD6E4911F CRC64;

Query Match 94.8%; Score 1625; DB 2; Length 379;  
 Best Local Similarity 94.9%; Pred. No. 6.2e-112;  
 Matches 319; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy	2	GDVDDAGDCSGARYNDWSDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARR	61
Db	44	GDVDDAGDCPGARYNDWSDDDDSYESKSIVWYPPWARIGTEAGTRARARARARATRARR	103
Qy	62	AVQKRASPNSDDTVLSPQELQVKLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	121
Db	104	AVQKRASPNSDDTVLSPQELQVKLCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLG	163
Qy	122	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLA	181
Db	164	GLPIVAKILNTRDPIVKEKALIVLNNLSVNAENQRRLKVMNQVCDDTVTSRLNSSVQLA	223
Qy	182	GLRLLTNMTVTNEYQHMLANSISDFTRLFSAGNEETKLQVLKLLNLAEQPAMTRELLRA	241
Db	224	GLRLLTNMTVTNEYQHILANSISDFTRLFSAGNEETKLQVLKLLNLAEQPAMTRELLRA	283
Qy	242	QVPSSLGSLFNKKENKEVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVC	301
Db	284	QVPSSLGSLFNKKEYKEVILKLLIIFENINDNFKWEENEPAQNHFSEGSPFFLKEFQVC	343
Qy	302	ADKXLGIESHHDFLVKVKGKFMAKLAEHMFPKSQE	337
Db	344	ADKVLGIESRHDQVRVKVGKFVAKLTERMFPKSQE	379

## RESULT 7

Q9P291

ID Q9P291 PRELIMINARY; PRT; 453 AA.  
 AC Q9P291;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE ALEX1 (Armadillo repeat containing, X-linked 1) (Hypothetical protein  
 DE FLJ90304).  
 GN Name=alex1; Synonyms=ARMCX1;

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21092608; PubMed=11162520;  
RA Kurochkin I.V., Yonemitsu N., Funahashi S., Nomura H.;  
RT "ALEX1, a novel human armadillo repeat protein that is expressed  
differentially in normal tissues and carcinomas.";  
RL Biochem. Biophys. Res. Commun. 280:340-347(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,  
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AB039670; BAA94603.1; -.  
DR EMBL; BC002691; AAH02691.1; -.  
DR EMBL; AK074785; BAC11208.1; -.  
DR PIR; JC7582; JC7582.  
DR InterPro; IPR008938; ARM.  
DR InterPro; IPR000225; Armadillo.  
DR InterPro; IPR006911; DUF634.  
DR Pfam; PF04826; DUF634; 1.  
DR PROSITE; PS50176; ARM\_REPEAT; 1.

## RESULT 8

Q9CX83  
ID Q9CX83 PRELIMINARY; PRT; 456 AA.  
AC Q9CX83;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched  
DE library, clone:3010033I09 product:similar to ALEX1 (ALEX1 PROTEIN)  
DE (3010033I09Rik protein) (Armadillo repeat containing, X-linked  
DE 1).  
GN Name=3010033I09Rik; Synonyms=Armcx1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).

RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N-3, and C57BL/6;  
RC TISSUE=Brain, Eye, and  
RC Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by  
RC biopsy.;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N-3;  
 RC TISSUE=Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by  
 RC biopsy.;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AK019405; BAB31705.1; -.  
 DR EMBL; BC021410; AAH21410.1; -.  
 DR EMBL; BC026488; AAH26488.1; -.  
 DR EMBL; BC068228; AAH68228.1; -.  
 DR MGD; MGI:1925498; 3010033I09Rik.  
 DR InterPro; IPR008938; ARM.  
 DR InterPro; IPR000225; Armadillo.  
 DR InterPro; IPR006911; DUF634.  
 DR Pfam; PF04826; DUF634; 1.  
 DR PROSITE; PS50176; ARM\_REPEAT; 1.  
 SQ SEQUENCE 456 AA; 50643 MW; 159EFAEF1B536406 CRC64;  
  
 Query Match 44.7%; Score 766.5; DB 2; Length 456;  
 Best Local Similarity 51.0%; Pred. No. 2.6e-48;  
 Matches 151; Conservative 51; Mismatches 81; Indels 13; Gaps 1;  
  
 QY 45 GTRARARARARATRARRAVQKRAS-----PNSDDTVLSPQELQKVLCLEMS 91  
 |:||||| :| |:||| | | :||| :||||| ::| :|:  
 Db 161 GSRARNRTSGVKRKNRSKSNKAPATAWPVRKGKFSPYKIDDILSAPDLQKVNLERT 220  
  
 QY 92 EKPYILEAALIALGNNAAYAFNRDIIRDGLGLPIVAKILNTRDPIVKEKALIVLNLSVN 151  
 |:| ||:|||||||:||::||:|||:||:||:|||:|||:|||:|||:|||:|||:  
 Db 221 NDPFTQEVALVTLGNNAAYSFNQNAIRELGGVPIIAKLIKTRDPIIREKTYNALNNLSVN 280

Qy 152 AENQRRLKVMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFFRLFS 211  
     :||| ::| |:::|||||: ||:|:||:|||||:|||:| :| ||| |  
 Db 281 SENQGKIKTYISQVCDDTMVCRLDSAVQMAGLRLLTNMTVTNHYQHLLSYSFPDFALLF 340  
  
 Qy 212 AGNEETKLQVLKLLLNLAEVPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENIN 271  
     || |::| :||::| |||||||: :||| | ||||: ::|::| :| :||| |  
 Db 341 LGNHFTKIQTMKLIINFTEVPAMTRELVSCKVPSLISLFNKEWDREILLNILTLEFENIN 400  
  
 Qy 272 DNFKWEENEPTQNQFGEGLFFLKEFQVCADKXLGIESHHDFLVKVKVGKFMAKL 327  
     || | | :: :| |||| | | | | : || | :||||| | : |||  
 Db 401 DNIKSEGLASSRKEFSRSSLFFLFKESGVCKKIKALASHKDLVVVKVVLTKL 456

## RESULT 9

AAH68228

ID AAH68228 PRELIMINARY; PRT; 456 AA.  
 AC AAH68228;  
 DT 01-JUN-2004 (TrEMBLrel. 27, Created)  
 DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RIKEN cDNA 3010033I09.  
 GN 3010033I09RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska-U., Smailus D.E., Schnurch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC068228; AAH68228.1; -.  
 SQ SEQUENCE 456 AA; 50643 MW; 159EFAEF1B536406 CRC64;

Query Match 44.7%; Score 766.5; DB 2; Length 456;  
 Best Local Similarity 51.0%; Pred. No. 2.6e-48;  
 Matches 151; Conservative 51; Mismatches 81; Indels 13; Gaps 1;

Qy	45 GTRARARARARATRARRAVQKRAS-----PNSDDTVLSPQELQKVLCLEMS 91
	:       :    : :        :   :     ::  :
Db	161 GSRARNRTSGVKRKNRSKSNKAPATAWPVRKGKFSPYKIDDILSAPDLQKVNLILERT 220
Qy	92 EKPYILEAALIALGNNAAYAFNRDIIRDGGGLPIVAKILNTRDPIVKEKALIVLNLSVN 151
	:       :        :  ::   :   :  :  :      :
Db	221 NDPFTQEVALVTLGNNAAYSFNQNAIRELGGVPIIAKLIKTRDPIIREKTYNALNNLSVN 280
Qy	152 AENQRRLKVMNQVCDDTITSRLNSSVQLAGRLLTNMTVTNEYQHMLANSISDFFRLLFS 211
	:    ::   ::       :   : :  :         :  :
Db	281 SENQGKIKTYISQVCDDTMVCRLDSAVQMAGLRLLTNMTVTNHYQHLLSYSFPDFALLF 340
Qy	212 AGNEETKLQLVLKLLLNAENPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENIN 271
	:  :  :         : :           : :: :  :  :
Db	341 LGNHFTKIQTMKLIINFTEPAMTRELVSCKVPSELISLFNKEWDREILLNILTLEFENIN 400
Qy	272 DNFKWEENEPTQNQFGEGLFFFLKEFQVCADKXLGIESHHDFLVKVKVGKFMALK 327
	:: :                :     :      :
Db	401 DNIKSEGLASSRKEFSRSSLFFLFKESGVCVKKIKALASHKDLVVVKVVLTKL 456

#### RESULT 10

Q7L311

ID Q7L311 PRELIMINARY; PRT; 632 AA.  
 AC Q7L311;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE ALEX2 protein.  
 GN Name=ARMCX2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta, and Skin;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DDJB databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Strausberg R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DDJB databases.  
DR EMBL; BC015926; AAH15926.1; -.  
DR EMBL; BC012541; AAH12541.1; -.  
DR InterPro; IPR008938; ARM.  
DR InterPro; IPR000225; Armadillo.  
DR InterPro; IPR006911; DUF634.  
DR Pfam; PF04826; DUF634; 1.  
DR SMART; SM00185; ARM; 1.  
SO SEQUENCE 632 AA; 65683 MW; 7627CBFFE61C329B CRC64;

Query Match 39.8%; Score 683; DB 2; Length 632;  
Best Local Similarity 45.3%; Pred. No. 5.9e-42;  
Matches 140; Conservative 56; Mismatches 91; Indels 22; Gaps 3;

Qy 18 WSDDDDNESKSIVWYPPWARIGTEAGTRARARARARATRARRAVQKRASPNSDDTVLS 77  
           |:| : ||:                                                                    |:||| | | :|  
 Db 345 WTDTESDSD-----SEPETORRGRRPV----AMOKRPFPEYEIDEILG 384

Qy 138 KEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLAGRLLLTNMTVTNEYQH 197  
|||||: :|||| | ||| ||:||||:| || : | |||:||: ||: ||||||:||:|||  
Pb 445 KEKALMANNIISENYENOGRIQVYMMNKVMDRIMASNLNSAVOWVGLKEITNMELITNDYQH 504

Qy 198 MLANSISDFRLFSAGNEETKLQLVLKLLNLAEVPAMTRELLRAQVPSLGSLFNKKENK 257  
P: :|:||:|:|||:| | :|:::||:| | |||| | ::| | |||:| | :|:  
E: 505 MLLNSISDFRLFSAGNEETKLQLVLKLLNLAEVPAMTRELLRAQVPSLGSLFNKKENK 564

Qy 258 EVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVCADKXLGIESHHDFLVK 317  
|:::| :||| ||| :| :| :|||:||| :| | :| :|||

Qy            318 VKVGKFMAK 326  
      | | | | : |

#### RESULT 11

RECORDED 11  
060367

ID 060367

ID 000287

AC O60267;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE KIAA0512 protein (Fragment).  
GN Name=KIAA0512;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98290545; PubMed=9628581;  
RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
RA Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. IX.  
RT The complete sequences of 100 new cDNA clones from brain which can  
RT code for large proteins in vitro.";  
RL DNA Res. 5:31-39(1998).  
DR EMBL; AB011084; BAA25438.2; -.  
DR PIR; T00084; T00084.  
DR InterPro; IPR008938; ARM.  
DR InterPro; IPR000225; Armadillo.  
DR InterPro; IPR006911; DUF634.  
DR Pfam; PF04826; DUF634; 1.  
DR SMART; SM00185; ARM; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 710 AA; 74240 MW; DCC56E38A038D780 CRC64;

Query Match 39.8%; Score 683; DB 2; Length 710;  
Best Local Similarity 45.3%; Pred. No. 6.9e-42;  
Matches 140; Conservative 56; Mismatches 91; Indels 22; Gaps 3;

Qy 18 WSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARARATRARRAVQKRASPNSDDTVLS 77  
|:| : ||: :| : | | | | :||| | | | :|  
Db 423 WTDTESDSD-----SEPETQRRGRGRRPV----AMQKRPF PYEIDEILG 462

Qy 78 PQELQKVLCVEMSEKPYILEAALIALGNNAAYAFNRDIIRD LGGLPIVAKILNTRDPIV 137  
::|:||| |:: |: |:| : ||: | ||| |: |: || | |||||||:| ::| | | :|  
Db 463 VRDLRKVLALLQKSDDPFIQQVALTLSNNANYSCNQETIRKLGGLPIIANMINKTDPHI 522

Qy 138 KEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQH 197  
|||||: :|||| | ||| ||:||||:| || :| |||:||: ||: ||||||:||:|||  
Db 523 KEKALMAMNNLSENYENQGRLQVYMNKVMDDIMASNLNSAVQVVGKFLTNMTITNDYQH 582

Qy 198 MLANSISDFFRLLFSAGNEETKLQVLKLLLNAENPAMTRELLRAQVPSSLGSLFNKKENK 257  
:| |||:|||| | | :|:||:| | ||| | :||| |||:| ||:|  
Db 583 LLVNSIANFFRLLSQGGGKIKVEILKILSNFAENPDMLKKLLSTQVPASFSSLYNSYVES 642

Qy 258 EVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFLKEFQVCADKXLGIESHHDFLVK 317  
|::: | :|| | || :| :| :|||: | || | :| ||| |||  
Db 643 EILINALTLFEIIYDNLRAEVF--NYREFNKGSLFYLCTTSGVCVKKIRALANHHDLLVK 700

Qy 318 VKVGKFMAK 326  
| || | : |  
Db 701 VKVIKLVNK 709

RESULT 12

BAA25438

ID BAA25438 PRELIMINARY; PRT; 710 AA.  
AC BAA25438;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE KIAA0512 protein (Fragment).  
GN KIAA0512.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98290545; PubMed=9628581;  
RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
RA Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. IX.  
RT The complete sequences of 100 new cDNA clones from brain which can  
RT code for large proteins in vitro.";  
RL DNA Res. 5:31-39(1998).  
DR EMBL; AB011084; BAA25438.2; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 710 AA; 74240 MW; DCC56E38A038D780 CRC64;

Query Match 39.8%; Score 683; DB 2; Length 710;  
Best Local Similarity 45.3%; Pred. No. 6.9e-42;  
Matches 140; Conservative 56; Mismatches 91; Indels 22; Gaps 3;

Qy 18 WSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARATRARRAVQKRASPNSDDTVLS 77  
|:| : ||: :| | :|| | :| ||| | :||| | | :| :|  
Db 423 WTDTESDSD-----SEPETQRRGRGRRPV----AMQKRPFPYEIDEILG 462

Qy 78 PQELQKVLCVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGGLPIVAKILNTRDPIV 137  
::|:|:||| |::| :|:| :||: | | ||| |:| ::| ||| :| :| | :|  
Db 463 VRDLRKVLALLQKSDDPFIQQVALTLSNNANYSNCQETIRKLGGGLPIIANMINKTDPHI 522

Qy 138 KEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQH 197  
|||||: :|||| | ||| ||:||||:| || :| |||:||: ||: |||||:||:|||  
Db 523 KEKALMAMNNLSENYENQGRLQVYMNKVMDDIMASNLNSAVQVVGLKFLTNTMTITNDYQH 582

Qy 198 MLANSISDFRRLFSAGNEETKLQVLKLLNLAENPAMTRELLRAQVPSSLGSLFNKKENK 257  
:| |||:|||| | | :| ::|:||:| | |||| | :||| |||:| ||:|  
Db 583 LLVNSIANFFRLLSQGGGKIKVEILKILSNFAENPDMLKKLLSTQVPASFSSLYNSYVES 642

Qy 258 EVILKLLVIFENINDNFKWEENEPTQNQFGEGLFFFKEFQVCADKXLGIESHHDFLVK 317  
|:::| :||| | || :| :| :|||:| ||| | :| :||| |||  
Db 643 EILINALTLEIIYDNLRAEVF--NYREFNKGSFLFYLCCTSGVCVKKIRALANHHDLLVK 700

Qy 318 VKVGKFMAK 326  
||| | :|  
Db 701 VKVIKLVNK 709

RESULT 13

Q9BTM6

ID Q9BTM6 PRELIMINARY; PRT; 308 AA.  
AC Q9BTM6;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE SVH protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC003586; AAH03586.1; -.  
DR InterPro; IPR008938; ARM.  
DR InterPro; IPR006911; DUF634.  
DR Pfam; PF04826; DUF634; 1....  
SQ SEQUENCE 308 AA; 33840 MW; B25A6C926BA5C101 CRC64;

Query Match 39.2%; Score 671.5; DB 2; Length 308;  
Best Local Similarity 49.0%; Pred. No. 1.6e-41;  
Matches 148; Conservative 50; Mismatches 91; Indels 13; Gaps 4;

Qy 37 WARIGTEAG-----TRARARA-RARATRARRAVQKRASPNSDDTVLSPQELQKVL 85  
| | | | || | | | | : : : : || || : ::|||:  
Db 9 WVAAGLLLGGAGACYCIYRLTRGRRRGDRELGIRSSKAEDLTDGSYDD-VLNNEQLQKLL 67  
Qy 86 CLVEMSEKPYILEAALIALGNNAAYAFNRDIIRD LGGLPIVAKILNTRDPIVKEKALIVL 145

|:| :| | |:| ||| |||||:: |: |||:|||:||| :| : :||||| |
 Db 68 YLLESTEDPVIIERALITLGNNAAFSVNQAIIRELGGIPIVANKINHSNQSIKEKALNAL 127  
 Qy 146 NNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLTNMTVTNEYQHMLANSISD 205  
 ||||| | | ::|:|:|||:| : |||:||||| |||||||::|:||| : |:  
 Db 128 NNLSVNVENQIKIKIYISQVCEVFSGSLNSAVQLAGLTLTNMTVTNDHQHMLHSYITD 187  
 Qy 206 FFRLFSAGNEETKLQVLKLLLNLAEVPAMTRELLRAQPSSLGSLFNKKENKEVILKLLV 265  
 |:: | | ||:|||||:||| | ||||| | | ||:|:|:||:  
 Db 188 LFQVLLTGNNGNTKVQVLKLLLNLSENPAMTEGLLRAQVDSSFLSLYDSHVAKEILLRVL 247  
 Qy 266 IFENINDNFKWEENEPTQNQFGEGLFFFKEFQVCADKXLGIESHHDFLVKVKVGKFMA 325  
 ::|:| : | | : | | ||||| | : || | : ||| || | :  
 Db 248 LFQNIKNCLKIEGHlavoptfTeGSLFFLL-HGEECAQKIRALVDHHDAEVKEVVTIIP 306  
 Qy 326 KL 327  
 |:  
 Db 307 KI 308

#### RESULT 14

Q8IZC1

ID Q8IZC1 PRELIMINARY; PRT; 308 AA.  
 AC Q8IZC1;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE SVH-B.  
 GN Name=SVH;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang R., Xing Z., Luan Z., Wu T., Wu X., Hu G.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY150853; AAN72315.1; -.  
 DR InterPro; IPR008938; ARM.  
 DR InterPro; IPR006911; DUF634.  
 DR Pfam; PF04826; DUF634; 1.  
 SQ SEQUENCE 308 AA; 33850 MW; 9F74718D8B96C102 CRC64;

Query Match 39.1%; Score 670.5; DB 2; Length 308;  
 Best Local Similarity 49.0%; Pred. No. 1.9e-41;  
 Matches 148; Conservative 50; Mismatches.. 91; Indels 13; Gaps 4;

Qy 37 WARIGTEAG-----TRARARA-RARATRARAVQKRASPNSDDTVLSPQELQKVL 85  
 | | | | | ||| | | | |: :: : : || | |: ::|:|:  
 Db 9 WVAAGLLLGAACYCIYRLTRGRRRGDRELGIRSSKSAEDLTDGSYDD-VLNaeQLQKLL 67  
 Qy 86 CLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDGLPIVAKILNTRDPIVKEKALIVL 145  
 |:| :| | |:| ||| |||||:: |: |||:|||:||| :| : :||||| |  
 Db 68 YLLESTEDPVIIERALITLGNNAAFSVNQAIIRELGGIPIVANKINHSNQSIKEKALNAL 127  
 Qy 146 NNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLTNMTVTNEYQHMLANSISD 205  
 ||||| | | ::|:|:|||:| : |||:||||| |||||||::|:||| : |:

Db 128 NNLSVNVENQIKIKIYISQVCEDVFSGPLNSAVQLAGLTLTNMTVTNDHQHMLHSYITD 187  
Qy 206 FFRLFSAGNEETKLQLKLLLNAENPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLV 265  
|:: || ||:|||||||:|||||| | || || || ||:: ||::|::|:  
Db 188 LFQVLLTGNGNTKVQLKLLNLSEN PAMTEGLLRAQVDSSFLSLYDSHVAKEILLRVLT 247  
Qy 266 IFENINDNFKWEENEPTQNQFGEGLFFFKEFQVCADKXLGIESHHDFLVKVKVGKFMA 325  
:|:|| : || : | | ||||| | : || | : ||| || || :  
Db 248 LFQNIKNCLKIEGHЛАVQPTFTEGSLFFLL-HGEECAQKIRALVDHHDAEVKEKVVTIIP 306  
Qy 326 KL 327  
|:  
Db 307 KI 308

RESULT 15

Q8BJ82

ID Q8BJ82 PRELIMINARY; PRT; 784 AA.  
AC Q8BJ82;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus 12 days embryo embryonic body between diaphragm region  
DE and neck cDNA, RIKEN full-length enriched library, clone:9430015G17  
DE product:weakly similar to KIAA0512 PROTEIN (ARMADILLO REPEAT PROTEIN  
DE ALEX2) (SIMILAR TO ARMADILLO REPEAT PROTEIN ALEX2).  
GN Name=3230401N03Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Embryonic body between diaphragm region and neck;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Embryonic body between diaphragm region and neck;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Embryonic body between diaphragm region and neck;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]



Db 537 VRDLRKVLALLQKSDDPFIQQVALTLSNNANYSCNQETIRKLGGLPIIANMINKTDPHI 596  
Qy 138 KEKALIVLNNLSVNAENQRRLKVMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQH 197  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 597 KEKALMAMNNLSENYENQGRLQVYMNKVMDDIMASNLNSAVQVVGLKFLTNMTITNDYQH 656  
Qy 198 MLANSISDFRRLFSAGNEETKLQVLKLLLNLAEVPAMTRELLRAQVPSSLGSLFNKKENK 257  
: | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 657 LLVNSIANFFRLLSQGGGKIKVEILKILSNFAENPDMLKKLLGTQVPSSFSSLNSYVES 716  
Qy 258 EVILKLLVIFENINDNFKEEPTQNQFGEGSLFFFKEFQVCADKXLGIESHHDFLVK 317  
| : | : | : | : | : | : | : | : | : | : | : |  
Db 717 EILINALTLFEIIFDNLRAEVF--NNREFNKGSLFYLCTTSGVCVKIRALANHHDLLVK 774  
Qy 318 VKVGKFMAK 326  
| : | : |  
Db 775 VKVIKLVNK 783

Search completed: January 7, 2005, 14:50:53  
Job time : 72.2668 secs